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(54) Title: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND BIOSENSORS OF CHEMICAL SENSANTS

(57) Abstract: The use of sensory G protein-coupled receptors that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants is described. The use of such products as a biosensor or a components thereof to detect, identify, measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant) is also described. The invention has application, for example, in the design and formulation of odorant and tastant compositions.

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## RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND BIOSENSORS OF CHEMICAL SENSANTS

### Cross Reference to Related Application

This application is related to U.S. Provisional Serial No. 60/213,812, filed June 22, 2000, and U.S. Serial No. 09/804,291, filed March 13, 2001, which are incorporated by reference in their entirety.

### Background of the Invention

#### Field of the Invention

The invention relates to the use of sensory G protein-coupled receptor complexes that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants. The invention also relates to the use of such products as a biosensor or component thereof to detect, to identify, to measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant). The invention has application, for example, in the design and formulation of odorant and tastant compositions.

#### Description of the Related Art

The olfactory and taste systems provide sensory information about the chemical environment. Olfactory receptors and taste receptors recognize, respectively, "odorants" and "tastants," collectively referred to as "sensants" or "sensory receptor ligands" herein. A "primary" sensant is an odorant or tastant ligand that substantially binds to sensory receptors with a ligand-binding site of a single amino acid sequence. Olfactory and taste receptors belong to the superfamily of seven-transmembrane guanyl nucleotide-binding proteins: such receptors are, however, also recognized as distinct families, or sub-genuses, of olfactory or taste

receptors (see Raming *Nature* 361:353, 1993). These receptors control diverse physiological functions such as media-ting signaling from an external chemical stimulus across the membrane containing the receptor into a cell, endocrine function, exocrine function, heart rate, lipolysis, and carbohydrate metabolism. Thus, the

5 dissection of these diverse functions into component signals is needed.

But the complexities of sensory perception of chemical sensants prevent easy translation of the olfaction and taste systems to a machine sensor. For example, U.S. Patent Nos. 5,675,070; 5,918,257; 5,928,609; and 6,085,576 disclose machine sensors that use various chemistries, but they do not take advantage of the specificity of

10 olfactory and taste receptors for their cognate ligands to produce a biosensor.

WO 00/15269 discloses methods and apparatus for odor reproduction. The total affinities of a specific odorant with a group of receptors was called the affinity fingerprint of the odorant. This odorant fingerprint was represented by a vector of affinity values. It was proposed to repro-duce an arbitrary odor by inputting its sensed

15 odorant fingerprint into a device, which has a palate of predetermined odorants and produces a composite odor using predetermined odorant finger-prints by minimizing the difference between vectors representing the sensed odorant fingerprint and the predetermined odorant fingerprints. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

WO 00/70343 discloses biosensors and sense replication systems using G-protein coupled receptors (GPCR). It was proposed to mimic the response of the G-protein signal transduction system by detecting the affinity of a stimulus to a plurality of GPCR, codifying such information into electronic signals, and reproducing the stimulus by converting the codified information into a combination of stimulant

25 entities. But this reference also does not teach or suggest the human olfactory receptors disclosed herein.

WO 01/27158 discloses olfactory receptors and their use to determine the correspondence between individual odorant receptors and particular odors. It was proposed that the interactions between an odor and olfactory receptors can be used to

30 represent the odor and to re-create it. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

Dissecting the function of sensory receptors by binding sensory receptors of a clone of cells expressing a single sensory receptor gene, fragmentation of sensory

receptors to provide ligand-binding or signal-transducing domains thereof, and construction of fusion sensory receptor proteins will separate the diverse physiological functions associated with sensory perception at the level of ligand-receptor binding. Furthermore, novel "primary sensants" that are identified and isolated by the methods described herein may be used to further define the function of the cognate sensory receptor by uniquely enhancing or, in the alternative, blocking stimulation of sensory receptors with a single ligand-binding domain.

The present invention addresses the need for better understanding of these ligand-receptor interactions by using a large set of identified sensory receptors. Even if the receptor set used is incomplete (*i.e.*, a partial set of all sensory receptors encoded in the genome), a large number of sensants will be detected. Moreover, redundancy in the chemical structures recognized by the sensory receptors or combinatorial processing of signals from different sensory receptors would allow broad coverage of chemically diverse sensants (*e.g.*, by selection of a representative class of sensory receptors). Also provided are, *inter alia*, methods for utilizing such sensory receptors and biosensors to simulate sensory perception. To analyze ligand-receptor interactions and their effects on cell signaling and the processing of those signals in sensory perception, specific sensants and their cognate receptor complexes are detected, identified, and measured under binding conditions. Fragrances and flavorings can be detected, identified, measured, and/or custom designed by the methods herein described. In addition, drugs that incorporate artificial odors and/or tastes can be formulated.

### Summary of the Invention

Large gene families encoding mammalian olfactory G-protein-coupled receptors (OLFR) and mammalian taste G-protein-coupled receptors (TASR) are known in the prior art or are disclosed herein. An object of the invention to provide fragments and variants of such OLFRs and TASRs which retain odorant- or tastant-binding activity, respectively. The large number of sensory receptors that are made available herein and now amendable to manipulation raises the confidence that a substantially complete, or at least functional, repertoire of sensory receptors is provided.



It is an object of the invention to provide nucleic acid sequences or molecules that encode such sensory receptors, or fragments or variants thereof. Another object is to provide expression vectors which include nucleic acid sequences that encode such sensory receptors, or fragments or variants thereof. It is yet another object of the invention to provide human or non-human cells which functionally express at least one of such sensory receptors, or fragments or variants thereof. Still another object is to provide sensory receptor fusion proteins or other polypeptides which include at least a fragment of at least one of such sensory receptors. In particular, fusions with reporter molecules or other heterologous amino acid sequences may maintain the original ligand-properties while changing the signaling properties to allow easier detection of sensant binding to the receptor (*e.g.*, change in fluorescent signal). Moreover, chimeric proteins or other polypeptides with altered ligand-binding and/or signaling properties can be made from two or more different sensory receptors by mixing domains.

15       The invention provides methods for representing the sensory perception of one or more chemicals (*e.g.*, a primary sensant or mixture thereof) and/or for predicting the sensory perception of one or more chemicals in a mammal (*e.g.*, human) using the aforementioned products. Given a known member of a ligand-receptor binding pair, one or both members of the pair (*i.e.*, ligand, receptor, or both) may be detected, identified, and/or measured under binding conditions.

20       Novel molecules or combinations of molecules which elicit a desired and predetermined sensory perception in a mammal (*e.g.*, human) can be generated by determining a value of sensory perception in a mammal for a known molecule or combination thereof; determining a value of sensory perception in a mammal for one or more unknown molecules or combinations thereof; comparing the value of sensory perception in a mammal for one or more unknown compositions to the value of sensory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined sensory perception in a mammal; and mixing two or more unknown molecules or combinations thereof to form a molecule or combination thereof that elicits a predetermined sensory perception in a mammal. The combining step yields a single molecule or a combination thereof that elicits a predetermined sensory perception in a mammal. In particular, primary odorants that uniquely bind to olfactory receptors with a single

ligand-binding domain may be such novel molecules. Variants thereof may be used (1) to enhance stimulation of a limited response by olfactory receptors with a single ligand-binding domain or (2) to block stimulation of olfactory receptors with a single ligand-binding domain to reduce or inhibit olfactory perception. An alternative method for identifying primary odorants is to identify the mutated receptors in genetic anosmias because that odorant would be expected to be recognized by only one or a few olfactory receptors affected by the mutation.

### Detailed Description of the Invention

#### 10 Perception of Chemical Sensants

U.S. Patent No. 5,691,188 describes how upon binding of ligand to receptor, the receptor presumably undergoes a conformational change leading to activation of the G protein. The G proteins are comprised of three subunits: a guanyl nucleotide binding  $\alpha$  subunit, a  $\beta$  subunit, and a  $\gamma$  subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the  $\alpha$  subunit. When GDP is bound, the G protein exists as a heterotrimer: the  $G\alpha\beta\gamma$  complex. When GTP is bound, the  $\alpha$  subunit dissociates from the heterotrimer, leaving a  $G\beta\gamma$  complex. When a  $G\alpha\beta\gamma$  complex operatively associates with an activated G protein coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of disso-ciation of the bound  $G\alpha$  subunit from the  $G\alpha\beta\gamma$  complex increases. The free  $G\alpha$  subunit and  $G\beta\gamma$  complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell. A high-resolution X-ray crystal structure is available for rhodopsin, a guanyl nucleotide binding protein, has been solved (Palczewski *et al.*, *Science* 289:739, 2000). Using this structure, the portions of the amino acid sequence of sensant receptors that are responsible for ligand binding can be identified.

30

#### Sensory Perception - Olfaction

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel *Sci. Amer.* 273:154, 1995). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer *Semin. Cell Biol.* 5:25, 1994). The human genome contains thousands of genes that encode a diverse repertoire of olfactory receptors (Rouquier *Nat. Genet.* 18:243, 5 1998; Trask *Hum. Mol. Genet.* 7:2007, 1998). An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that sensory receptors belong to a 10 multigene family with over a thousand members, and the odorant receptors number at least 500 to 1,000. Moreover, each sensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it 15 expresses.

#### Sensory Perception - Taste

Mammals are believed to have five basic taste modalities: sweet, bitter, sour, salty, and umami (the taste of monosodium glutamate). See, e.g., Kawamura *et al.*, 20 *Introduction to Umami: A Basic Taste* (1987); Kinnamon *et al.*, *Ann. Rev. Physiol.*, 54:715, 1992; Lindemann, *Physiol. Rev.*, 76:718, 1996; Stewart *et al.*, *Am. J. Physiol.*, 272:1, 1997. Numerous physiological studies in animals have shown that taste receptor cells may selectively respond to different chemical stimuli. See, e.g., Akabas *et al.*, *Science*, 242:1047, 1988; Gilbertson *et al.*, *J. Gen. Physiol.*, 100:803, 1992; 25 Bernhardt *et al.*, *J. Physiol.*, 490:325, 1996; Cummings *et al.*, *J. Neurophysiol.*, 75:1256, 1996.

In mammals, taste receptor cells are assembled into taste buds that are distributed into different papillae in the tongue epithelium. Circumvallate papillae, found at the very back of the tongue, contain hundreds, e.g., mice, to thousands, e.g., 30 human, of taste buds. By contrast, foliate papillae, localized to the posterior lateral edge of the tongue, only contain dozens to hundreds of taste buds. Moreover, fungiform papillae contain only a single or a few taste buds, and are at the front of the tongue.

AC010814, AC018700, AC021304, AC008620, AC011537, AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, 5 AP001803, AP001804, AL353767, AP001884, AC026083, AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, 10 AP002826, AL359636, AL391534, AC055731, AC076959, AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes. Similarly, genes encoding five and thirty-six (36) distinct, novel human T1R and T2R taste receptors, respectively, have been identified in genome 15 sequence databases.

Alternatively, nucleic acids encoding the sensory receptors and other related polypeptides can be isolated from a variety of sources, genetically engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 00/35374, which is herein incorporated by reference in its entirety.

20 These nucleic acids provide probes for the identification of cells expressing sensory receptors, as the nucleic acids are specifically expressed in such cells. They can also serve as tools for the generation of sensory topographical maps that elucidate the relationship between cells expressing sensory receptors and sensory neurons leading to particular regions of the brain. Furthermore, the nucleic acids and the 25 polypeptides they encode can be used as probes to elucidate olfactant- or tastant-induced behaviors.

Nucleic acid molecules encoding a sensory receptor comprising a nucleic acid sequence that is at least 75%, 85%, 90%, 95%, or 99% identical to a nucleic acid sequence selected from those known in the prior art or disclosed herein are considered 30 variants. Other nucleic acid molecules comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence at least 75%, 85%, 90%, 95%, or 99% identical to an amino acid sequence selected from those known in the prior art or disclosed herein are also considered variants. Further variants contain amino acid

sequence differences in at most ten, five, four, three, two, or one amino acid residue(s).

Exemplary nucleic acid sequences may be selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID

NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288,  
 SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID  
 NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306,  
 SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID  
 5 NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324,  
 SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID  
 NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342,  
 SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID  
 NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360,  
 10 SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID  
 NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378,  
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 15 NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414,  
 SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID  
 NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432,  
 SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID  
 NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450,  
 20 SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID  
 NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468,  
 SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID  
 NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486,  
 SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID  
 25 NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504,  
 SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512.

Nucleic acid molecule comprising a nucleic acid sequence that encodes a  
 fragment of a polypeptide having an amino acid sequence selected from those known  
 in the prior art or disclosed herein; wherein the fragment is at least ten, 20, 30, 50, 70,  
 30 100, or 150 amino acid residues in length, are useful as probes, primers, and to  
 construct hybrids or chimerae.

Polypeptides comprising an amino acid sequence that is at least 90%, 95%,  
 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from those

known in the prior art or disclosed herein are considered variants. Further variants contain amino acid sequence differences in at most ten, five, four, three, two, or one amino acid residue(s). Other polypeptides comprising a fragment of a polypeptide having an amino acid sequence selected from those known in the prior art or disclosed  
5 herein; wherein the fragment is at least 40, 60, 80, 100, 150, 200, or 250 amino acid residues in length, are useful as specific binders of sensants, competitive binders, antigens, and to construct hybrids or chimerae.

Exemplary amino acid sequences may be selected from the group consisting of  
10 SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ  
15 ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109,  
20 SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID  
25 NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199,  
30 SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,

SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Also provided are methods of screening for modulators, *e.g.*, activators, inhibitors, stimulators, enhancers, agonists, and antagonists, of the sensory receptors,



or fragments or variants thereof. Such modulators of signal transduction are useful for pharmacological or genetic modulation of signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of sensory cell activity. These modulator compounds can then be used in the pharmaceutical, food, and cosmetic industries to customize odorants or tastants.

Thus, the invention provides assays for sensory modulation, where the sensory receptors, or fragments or variants thereof, act as direct or indirect reporter molecules for the effect of modulators on signal transduction. Sensory receptors, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo*, and *ex vivo*. In one embodiment, sensory receptors, or fragments or variants thereof, can be used as indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g., Mistili et al., Nature Biotech.*, 15:961, 1997). In another embodiment, the sensory receptors, or fragments or variants thereof, can be expressed in host cells, and modulation of signal transduction via sensory receptor activity can be assayed by measuring changes in  $\text{Ca}^{2+}$  levels.

Methods of assaying for modulators of signal transduction include *in vitro* ligand binding assays using the sensory receptors, or fragments or variants thereof. More particularly, such assays can use the sensory receptors; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G-protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular  $\text{Ca}^{2+}$  levels; and neurotransmitter release.

The invention also provides for methods of detecting sensory receptor nucleic acid and protein expression, allowing for the investigation of taste transduction regulation and specific identification of sensory receptor cells. The sensory receptors, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying a sensory receptor cells. Sensory receptor cells can be identified using techniques such as reverse transcription and amplification

of mRNA, isolation of total RNA or poly A<sup>+</sup> RNA, Northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, Western blots, and the like.

A. Identification and Characterization of Sensory Receptors

5       The amino acid sequences of the sensory receptors and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

10       For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as  
15       described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

20       A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment  
25       of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970, by the search for similarity method of Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and  
30       TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J Mol. Biol.* 215:403, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J. Mol. Biol.* 215:403, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (see, e.g., Figure 2). PILEUP uses a simplification of the progressive

alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351, 1987. The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151, 1989. The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, e.g., version 7.0 (Devereaux *et al.*, *Nucl. Acids Res.* 12:387, 1984) encoded by the genes were derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the olfactory receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative sensory receptor proteins generally having lengths of about 300 to about 400 amino acid residues that contain seven transmembrane domains, as predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the 256 sensory receptors identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all 256 sequences contain very close matches to the following consensus amino acid motifs (Mombaerts, 1999; Pilpel, 1999): LHTPMY in intracellular loop 1, MAYDRYVAIC at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5,

FSTCSSH in the beginning of transmembrane domain 6, and PMLNPF in transmembrane domain 7. Combination of all the above mentioned structural features of the 256 genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

- 5 As noted above, complete or partial sequences of numerous human and other eukaryotic sensory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human sensory receptors, which suggests their different specificity in sensant recognition. Therefore, these novel sensory receptors and their genes can be used, alone or in combination
- 10 with known sensory receptors, in developing detection systems and assays for chemically distinct types of sensants not recognized by the known sensory receptors, as well as for diagnostic and research purposes.

B. Definitions

- The terms "purified," "substantially purified," and "isolated" as used herein
- 15 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
- 20 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
- 25 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or
- 30 proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

The terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, sensant-binding sequences of the invention) *in vivo* or *in vitro*.

The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and taste receptors each belong to this super-family. Seven-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, *i.e.*, drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated sensory, particularly olfactory or taste, receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of vectors that incorporate the amplified sensant-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding a sensory receptor.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, *i.e.*, oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like

structures with synthetic backbones, *see e.g.*, *Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Anti-sense Strategies*, Annals of the N.Y. Academy of Sciences, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan (1993) *J. Med. Chem.* 36:1923-1937; *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata (1997) *Toxicol. Appl. Pharmacol.* 144:189-197; Strauss-Soukup (1997) *Biochemistry* 36:8692-8698; Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156.

The term sensory receptor "ligand-binding region" refers to sequences derived from a sensory receptor that substantially incorporates transmembrane domains II to VII (TM II to VII). The domain may be capable of binding a sensant.

The terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the poly-peptide's (the conservative variant's) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, etc.) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing function-ally similar amino acids are well known in the art.

For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): Ala/Gly or Ser; Arg/Lys; Asn/Gln or His; Asp/Glu; Cys/Ser; Gln/Asn; Gly/Asp; Gly/Ala or Pro; His/Asn or Gln; Ile/Leu or Val; Leu/Ile or val; Lys/Arg or Gln or Glu; Met/Leu or Tyr or Ile; Phe/Met or Leu or Tyr; Ser/Thr; Thr/Ser; Trp/Tyr; Tyr/Trp or Phe; Val/Ile or Leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g.*, Creighton, *Proteins*, W.H. Freeman, 1984; Schultz & Schimer, *Principles of Protein Structure*, Springer-Verlag, 1979). One of skill in the art will appreciate that the above-identified substitutions are not the only possible

conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains or sensant-binding domains or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH<sub>2</sub>- for -C(=O)-NH-), aminomethylene (CH<sub>2</sub>-NH), ethylene, olefin (CH=CH), ether (CH<sub>2</sub>-O), thioether (CH<sub>2</sub>-S), tetrazole (CN<sub>4</sub>), thiazole, retroamide, thioamide, or ester (see, *e.g.*, Spatola (1983) in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, "Peptide Backbone Modifications,"



Marcell Dekker, NY). A polypeptide can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

The term "transmembrane domain" means a polypeptide domain that can completely span the plasma membrane. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below.

### C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the sensory receptors, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (e.g., promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature. See, *e.g.*, Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I, Theory and Nucleic Acid Preparation*, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, *e.g.*, analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, *e.g.*, fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), immunofluorescent assay, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (*e.g.*, SDS-PAGE),

RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (*PCR Protocols, a Guide to Methods and Applications*, ed. Innis, Academic Press, NY, 1990 and *PCR Strategies*, ed. Innis, Academic Press, NY, 1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560, 1989; Landegren, *Science* 241:1077, 1988; Barringer, *Gene* 89:117, 1990); transcription amplification (see, e.g., Kwok, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989); and, self-sustained sequence replication (see, e.g., Guatelli, *Proc. Natl. Acad. Sci. USA* 87:1874, 1990); Q Beta replicase amplification (see, e.g., Smith, *J. Clin. Microbiol.* 35:1477, 1997); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257, 1996) and other RNA polymerase mediated techniques (e.g., NASBA, Cingene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307, 1987; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563, 1995.

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, e.g., U.S. Patent No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the sensant-binding region-coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted sensant-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I

and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify sensant-binding regions of olfactory receptor proteins. These domain regions may vary for different sensants, and more particularly odorants; thus, what may be a minimal binding region for one sensant, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane sensory receptor.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII.

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3'). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify a transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL, encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CA-NGT-3'. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g., Rose, Nucl. Acids Res.* 26:1628, 1998; Singh, *Biotechniques* 24:318, 1998).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866, 1997. Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950, 1998). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, Proc. Natl. Acad. Sci. USA* 95:4258, 1998). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see above*). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-  
3' and  
5'-  
GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-  
3'.
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-  
3' and  
5'-  
GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-  
3'.
- (c) 5'-  
GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)  
GG-3' and  
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)  
TT(C/T)(C/T)T-3'.

Nucleic acids that encode ligand-binding regions of olfactory receptors are generated by amplification (*e.g.*, PCR) of appropriate nucleic acid sequences using degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova, *Proc. Natl. Acad. Sci. USA* 93:9858, 1996). Shirley, *Eur. J. Biochem.* 32:485, 1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211, 1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*,

antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260, 1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.

5           Hybrid protein-coding sequences comprising nucleic acids sensory receptors fused to the translocation sequences described herein may be constructed. Also provided are hybrid receptors comprising the translocation motifs and ligand-binding domains of sensory receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, *e.g.*, transcription and translation  
10   initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can  
15   also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227, 1998). Receptor genes are normally expressed in a small subset of  
20   neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

          Fusion proteins, either having C-terminal or, more preferably, N-terminal  
25   translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized  
30   metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289, 1998), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615, 1997); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a nucleic acid sequence encoding a polypeptide linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787, 1995), and an amino terminal translocation domain. The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, *see, e.g., Kroll, DNA Cell. Biol.* 12:441, 1993).

Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent literature. *See, e.g., Roberts, Nature* 328:731, 1987; Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10, 1995; Sambrook; Tijssen; Ausubel. Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g., episomal expression systems*). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin*) or herbicide resistance (*e.g., chlorosulfuron or Basta*) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g., Blondelet-Rouault, Gene* 190:315, 1997; Aubrecht, *J. Pharmacol. Exp. Ther.* 281:992, 1997). Because



selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a sensant-binding domain within any 7-transmembrane polypeptide. Seven-transmembrane receptors belong to a superfamily of trans-membrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-trans-membrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (e.g., TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969, 1999; Rost, *Protein Sci.* 4:521, 1995. Periodicity detection enhancement and alpha helical periodicity index can be done as by, e.g., Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, see, e.g., Peitsch, *Receptors Channels* 4:161, 1996; Cronet, *Protein Eng.* 6:59, (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, e.g., TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (e.g., PCR) from mRNA of or cDNA derived from, e.g., olfactory receptor-expressing neurons or genomic DNA.

Libraries of sensory receptor ligand-binding TM domain sequences can include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, e.g., homology modeling, Fourier analysis and helical periodicity (see, e.g., Pilpel *supra*), as described above. Using this information sequences flanking the seven

domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of, for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the sensory receptors described herein, coupled to additional amino acids representing all or part of another G protein receptor, preferably a member of the 7-transmembrane superfamily. These chimerae can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the 7-transmembrane protein described herein, and the remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand binding domain, an extracellular domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous CGPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, e.g., green fluorescent protein,  $\beta$ -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to a sensory receptor disclosed herein can be isolated using the nucleic acid probes described above. Alternatively, expression libraries can be used to isolate sensory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against a sensory receptor-derived polypeptide, which also recognize and selectively bind to the sensory receptor homolog.

Also within the scope of the invention are host cells for expressing the sensory receptors, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the sensory receptors, fragments, or variants thereof, the nucleic acid sequence of interest is subcloned into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable prokaryotic and eukaryotic expression systems are well known in the art and described, e.g., in Sambrook *et al.*

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasmid vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g., Sambrook et al.*). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.,* WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

#### D. Immunological Detection of Sensory Receptor Polypeptides

In addition to the detection of sensory receptor genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect

sensory receptors, *e.g.*, to identify olfactory receptor cells, and variants of sensory receptor family members. Immunoassays can be used to qualitatively or quantitatively analyze the sensory receptors. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

5           1.       Antibodies to sensory receptor family members

              Methods of producing polyclonal and monoclonal antibodies that react specifically with a sensory receptor family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology*, 1991; Goding, *Monoclonal Antibodies: Principles and Practice*, 2d ed., 1986; Harlow & Lane, *supra*; and Kohler & Milstein, *Nature*, 256:495, 1975). Such techniques include antibody preparation by  
10       selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (*see, e.g.*, Huse *et al.*, *Science*, 246:1275, 1989; Ward *et al.*, *Nature*, 341:544, 1989).

15           A number of sensory receptor-comprising immunogens may be used to produce antibody specifically reactive with a sensory receptor family member. For example, a recombinant sensory receptor protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the sensory receptor family.

20       Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring  
25       protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

              Methods of production of polyclonal antibodies are known to those of skill in  
30       the art. Mice, hamsters, rats, guinea pigs, rabbits, goats, or chickens is immunized with the protein using an adjuvant (*e.g.*, Freund's adjuvant) and a standard immunization protocol with periodic boosts. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of

reactivity to the sensory receptor. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (see Harlow & Lane, *supra*).

5            Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (see Kohler & Milstein, *Eur. J. Immunol.*, 6:511, 1976). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, retroviruses, or other  
10        methods well known in the art. Colonies arising from single clones of immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a  
15        monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275, 1989.

            Monoclonal antibodies or polyclonal sera are collected and titered against antigen in an immunoassay, for example, a solid phase immunoassay with the antigen  
20        immobilized on a solid support. Typically, polyclonal antisera with a titer of  $10^4$  or greater are selected and tested for their cross reactivity against non-sensory receptor proteins, or even other sensory receptor family members or other related proteins from other organisms, using a competitive binding immuno-assay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a  $K_d$  of at least about 0.1  
25        mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

            Once sensory receptor family member specific antibodies are available, individual sensory receptor proteins can be detected by a variety of immunoassay methods. For a review of immuno-nological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed., 1991). Moreover, the  
30        immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

## 2. Immunological binding assays

Sensory receptor proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patent Nos. 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general  
5 immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed., 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case a sensory receptor family member or an antigenic subsequence thereof). The antibody (e.g., anti-sensory  
10 receptor) may be produced by any of a number of means well known to those of skill in the art and as described above.

Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent  
15 may be a labeled sensory receptor polypeptide or a labeled anti-sensory receptor antibody. Alternatively, the labeling agent may be a third moiety, such a secondary antibody, that specifically binds to the antibody/sensory receptor complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding  
20 immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (see, e.g., Kronval *et al.*, *J. Immunol.*, 111:1401, 1973; Akerstrom *et al.*, *J. Immunol.*, 135:2589, 1985). The labeling agent can be modified with a detectable moiety, such as biotin, to which  
25 another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the  
30 incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting a sensory receptor protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays directly measure the amount of antigen. In one preferred "sandwich" assay, for example, the anti-sensory receptor antibodies are bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the sensory receptor protein present in the test sample. The sensory receptor protein thus immobilized is then bound by a labeling agent, such as a second anti-sensory receptor antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.*, streptavidin, to provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of sensory receptor protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) sensory receptor protein displaced (competed away) from an anti-sensory receptor antibody by the unknown sensory receptor protein present in a sample. In one competitive assay, a known amount of sensory receptor protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the sensory receptor. The amount of exogenous sensory receptor protein bound to the antibody is inversely proportional to the concentration of sensory receptor protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of sensory receptor protein bound to the antibody may be determined either by measuring the amount of sensory receptor protein present in a sensory receptor/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of sensory receptor protein may be detected by providing a labeled sensory receptor molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known sensory receptor protein is immobilized on a solid substrate. A known amount of anti-sensory receptor antibody is added to the sample, and the sample is then contacted with the immobilized sensory receptor. The amount of anti-sensory receptor antibody bound to the known immobilized sensory receptor protein is

inversely proportional to the amount of sensory receptor protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, sensory receptor proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the sensory receptor polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percentage cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the sensory receptor family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or poly-morphic variant of a sensory receptor family member, to the immunogen protein (*i.e.*, sensory receptor protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to



specifically bind to the polyclonal antibodies generated to a sensory receptor immunogen.

Antibodies raised against sensory receptor conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the sensory receptor family, but not to GPCRs from other families. Polyclonal antibodies that specifically bind to a particular member of the sensory receptor family, can be made by subtracting out cross-reactive antibodies using other sensory receptor family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human T2R01 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OLFR1 or mouse OLFR1.

d. Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of sensory receptor protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the sensory receptor protein. The anti-sensory receptor polypeptide antibodies specifically bind to the sensory receptor poly-peptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-sensory receptor antibodies.

Other assay formats include liposome immunoassays (LIA) using liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34, 1986).

e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein

compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f. Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immuno-assays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, bio-chemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS™, fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g.,  $^3\text{H}$ ,  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^{32}\text{P}$ ), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, etc.).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to another molecules (e.g., streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a sensory receptor protein, or secondary antibodies that recognize anti-sensory receptor.

The molecules can also be conjugated directly to signal generating compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone,

*etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, see U.S. Patent No. 4,391,904.

Methods for detecting labels are well known. Thus, for example, where the label is a radioactive label, it may be detected using a scintillation counter or with photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluoro-chrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, with photographic film, or using electronic detectors such as charge coupled devices (CCDs) or photomultipliers. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

#### E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian sensory, and more particularly, olfactory receptor of the invention, both *in vitro* and *in vivo* are described below, as are methods and compositions for determining whether a test compound is neurotoxic to an olfactory neuron expressing an olfactory transmembrane receptor polypeptide. Any aspect of cell physiology can be monitored to assess the effect of sensant-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical

stimuli into electrical signals. An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and  
5 other cognate G-proteins, and modulation of diverse channels by Gi and other G-proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The sensory receptor protein of the assay will typically be selected from a  
10 natural poly-peptide or conservatively modified variant thereof. Generally, the amino acid sequence identity will be at least 75%, 85%, 90%, 95%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of a sensory receptor protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand binding domain, subunit association domain, active site, and the like.  
15 Either the sensory receptor protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein.

Modulators of sensory receptor activity can be tested using sensory receptor polypeptides as described above, either recombinant or naturally occurring. Protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell,  
20 expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

#### 1. *In vitro* binding assays

Sensory perception can also be examined *in vitro* with soluble or solid state reactions, using a full-length sensory receptor-GPCR or a chimeric molecule such as  
25 an extracellular domain or transmembrane region, or combination thereof, of a sensory receptor covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of a sensory receptor. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or  
30 solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a sensory receptor polypeptide, as well an additional sequence that facilitates the localization of the

sensory receptor to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein.

Ligand binding to a sensory receptor protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbence, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties. Sensory receptors with large (*e.g.*, approximately 600 amino acid residues) extracellular N-terminal segments. These N-terminal segments are thought to form ligand-binding domains, and are therefore useful in biochemical assays to identify sensory receptor agonists and antagonists. Similar assays have been used with other GPCRs, such as the metabo-tropic glutamate receptors (*e.g.*, Han & Hampson, *J. Biol. Chem.* 274:10008, 1999). These assays might involve displacing a radioactively or fluorescently labeled ligand, and measuring changes in intrinsic fluorescence or changes in proteolytic susceptibility, *etc.*

Receptor-G-protein interactions can also be examined. For example, binding of the G-protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

## 2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor sensant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation, or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the sensory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nano-seconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the sensory receptors of the invention, fluorescence-labeled sensants or auto-fluorescent sensants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where  $\parallel$  is the intensity of the emission light parallel to the excitation light plane and  $\perp$  is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For

example, the Beacon® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley *J. Anal. Toxicol.* 5, 236, 1981 which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity ( $\eta$ ), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$\text{Rotational Relaxation Time} = \frac{3\eta V}{RT}$$

The rotational relaxation time is small ( $\approx 1$  nanosecond) for small molecules (e.g., fluorescein) and large ( $\approx 100$  nanoseconds) for large molecules (e.g., immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

### 3. Soluble and solid state high throughput assays

In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand binding domain, an extracellular domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous protein to create a chimeric molecule; a sensory receptor protein; or a cell or tissue expressing a sensory receptor protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the domain, chimeric molecule, sensory receptor protein, or cell or tissue expressing the sensory receptor is attached to a solid phase substrate.

In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the taste transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,



describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

#### 4. Computer-based assays

5 Yet another assay for compounds that modulate sensory receptor protein activity involves computer assisted drug design, in which a digital or analog processing system is used to generate a three-dimensional structure of a sensory receptor protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a  
10 preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g.*, ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering  
15 protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a sensory receptor polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of those described herein, or fragments or variants thereof.

20 The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*,  
25 magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.

The amino acid sequence represents a primary structure that encodes the  
30 information necessary to form the secondary, tertiary and quaternary structure of the protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent

accessible surfaces, and hydrogen bonding. Secondary energy terms include van der Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the sensory receptor protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of sensory receptor genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used to identify patients having such mutated genes. Identification of the mutated sensory receptor genes involves receiving input of a first nucleic acid or amino acid sequence of a sensory receptor gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once

odorant dependent activation monitored. Control samples (untreated with activators or inhibitors) are assigned a relative sensory receptor activity value of 100. Inhibition of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a sensory receptor protein. One means to determine changes in cellular polarization is by measuring changes in current, and thereby measuring changes in polarization, with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575, 1997). Whole cell currents are conveniently determined using the standard. Other known assays include: assays to measure ion flux using radiolabeled or fluorescent probes such as voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67, 1988; Gonzales & Tsien, *Chem. Biol.*, 4:269, 1997; Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185, 1991; Holevinsky *et al.*, *J. Membrane Biology*, 137:59, 1994). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, Northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as  $\text{Ca}^{2+}$ , IP3, cGMP, or cAMP.

Preferred assays for G-protein coupled receptors include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G-protein coupled receptors as negative or positive controls to assess activity of tested compounds. In assays for identifying modulatory compounds (*e.g.*, agonists,

antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G-protein coupled receptors, promiscuous G-proteins such as  $G\alpha 15$  and  $G\alpha 16$  can be used in the assay of choice (Wilkie *et al.*, *Proc. Natl. Acad. Sci.*, 88:10049, 1991). Such promiscuous G-proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, increases in second messengers such as IP<sub>3</sub>, which releases intracellular stores of calcium ions. Activation of some G-protein coupled receptors stimulates the formation of inositol triphosphate (IP<sub>3</sub>) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature* 312:315, 1984). IP<sub>3</sub> in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP<sub>3</sub> can be used to assess G-protein coupled receptor function. Cells expressing such G-protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (see, *e.g.*, Altenhofen *et al.*, *Proc. Natl. Acad. Sci.*, 88:9868, 1991 and Dhallan *et al.*, *Nature* 347:184, 1990). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*, certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors,

serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, sensory receptor protein activity is measured by expressing a sensory receptor gene in a heterologous cell with a promiscuous G-protein that links the receptor to a phospholipase C signal transduction pathway (see Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995). Optionally the cell line is HEK-293 (which does not naturally express sensory receptor genes) and the promiscuous G-protein is Gal 5 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by measuring changes in intracellular  $\text{Ca}^{2+}$  levels, which change in response to modulation of the sensory receptor signal transduction pathway via administration of a molecule that associates with a sensory receptor protein. Changes in  $\text{Ca}^{2+}$  levels are optionally measured using fluorescent  $\text{Ca}^{2+}$  indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be measured using immunoassays. The method described in Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995, may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159, 1994, may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent No. 4,115,538, herein incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent No. 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing a sensory receptor protein of interest is contacted with a test compound for a sufficient time to

effect any interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent No. 5,436,128, herein incorporated by reference. The reporter genes can be, e.g., chloramphenicol acetyltransferase, luciferase,  $\beta$ -galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (see, e.g., Mistili & Spector, *Nature Biotech.* 15:961, 1997).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the sensory receptor protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the sensory receptor protein of interest.

#### 6. Transgenic non-human animals expressing sensory receptors

Non-human animals expressing one or more sensory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of translocation domains in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize

odorants/ligands that can bind to a specific or sets of receptors. Such vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

- 5        Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses.
- 10      When electrodes are located on the olfactory bulb surface it is possible to record stable responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287, 1997). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of
- 15      one turbinate bone or were placed in corresponding positions on four turbinate bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950, 1997; Scott, *J. Neuro-physiol.* 75:2036, 1996; Ezech, *J. Neurophysiol.* 73:2207, 1995. In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and
- 20      medial surface of the turbinates (*see, e.g.*, Youngentob, *J. Neuro-physiol.* 73:387, 1995). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1, 1991).

- The sensory receptor sequences of the invention can be for example expressed
- 25      in animal nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *Proc. Natl. Acad. Sci. USA* 96:4040, 1999.

- The endogenous olfactory receptor genes can remain functional and wild-type
- 30      (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97, 1997). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotential embryonic stem (ES) cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53, 1998); Moreadith, *J. Mol. Med.* 75:208, 1997; Tojo, *Cytotechnology* 19:161, 1995; Mudgett, *Methods Mol. Biol.* 48:167, 1995; Longo, *Transgenic Res.* 6:321, 1997; U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries can also be used as reagents to produce "knockout" human cells and their progeny.

#### F. Modulators

The compounds tested as modulators of a sensory receptor family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of a sensory receptor gene. Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by



automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO),  
5 Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such  
10 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

15 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a  
20 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not  
25 limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka, *Int. J. Pept. Prot. Res.* 37:487, 1991; and Houghton *et al.*, *Nature* 354:84, 1991). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (e.g., WO 91/19735), encoded peptides (e.g., WO 93/20242), random bio-oligomers (e.g., WO 92/00091),  
30 benzodiazepines (e.g., U.S. Patent No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci.* 90:6909, 1993), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568, 1992), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer.*

Moreover, a method is provided for simulating a fragrance or flavor sensed by a mammal (*e.g.*, human), comprising: for each of a plurality of sensory receptors, or fragments or variants thereof, ascertaining the extent to which the sensory receptor interacts with the fragrance and/or flavor; and combining a plurality of compounds, each having a previously-determined interaction with one or more of the sensory receptors, in amounts that together provide a stimulation profile that mimics the profile for the fragrance and/or flavor. Interaction of a fragrance and/or flavor with a sensory receptor can be determined using any of the binding or reporter assays described herein. The interactions can be aggregated or a profile generated using known signal processing techniques (*e.g.*, a neural network) as described below. The sensory receptor, or fragments or variants thereof (*e.g.*, fusion proteins with reporters, chimeric proteins) may be expressed in cells; otherwise, ligand-binding domain(s) may be fixed to a substrate (*e.g.*, planar, bead, or fiber) that is solid or porous. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80%, 90%, 95%, 99% or all of the receptors that are substantially stimulated by the fragrance or flavor.

In yet another aspect of the invention, a method is provided in which a plurality of standard compounds are tested against a plurality of sensory receptors, or fragments or variants thereof, to ascertain the extent to which the sensory receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on data storage medium. The method may further comprise providing a desired receptor-stimulation profile for an odor and/or taste; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the odor and/or taste.

A further aspect of the invention is to provide a method for representing sensory perception of a particular odor and/or taste in a mammal (*e.g.*, human), comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  sensory receptors of the mammal; where  $n$  is greater than or equal to 5,  $n$  is

greater than or equal to 10,  $n$  is greater than or equal to 20,  $n$  is greater than or equal to 50,  $n$  is greater than or equal to 75,  $n$  is greater than or equal to 100,  $n$  is greater than or equal to 125,  $n$  is greater than or equal to 150,  $n$  is greater than or equal to 175,  $n$  is greater than or equal to 200,  $n$  is greater than or equal to 225,  $n$  is greater than or equal to 250,  $n$  is greater than or equal to 275,  $n$  is greater than or equal to 300,  $n$  is greater than or equal to 325, or  $n$  is greater than or equal to 350; and generating from the values a quantitative representation of sensory perception. The sensory receptors may be a receptor disclosed herein, or fragments or variants thereof. The representation may constitute a point or a volume in  $n$ -dimensional space, may constitute a graph or a spectrum, or may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced sensory receptors, or fragments or variants thereof, with a composition and quantitatively measuring the interaction of the composition with the receptors. The maximum number of taste receptors that are needed to mimic the native repertoire (e.g., about 50) may be less than the maximum number of olfactory receptors that are needed (e.g., about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

It is yet another aspect of the invention to provide a method for predicting the sensory perception in a mammal (e.g., human) generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in the mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  sensory receptors of the mammal; where  $n$  is greater than or equal to 5,  $n$  is greater than or equal to 10,  $n$  is greater than or equal to 20,  $n$  is greater than or equal to 50,  $n$  is greater than or equal to 75,  $n$  is greater than or equal to 100,  $n$  is greater than or equal to 125,  $n$  is greater than or equal to 150,  $n$  is greater than or equal to 175,  $n$  is greater than or equal to 200,  $n$  is greater than or equal to 225,  $n$  is greater than or equal to 250,  $n$  is greater than or equal to 275,  $n$  is greater than or equal to 300,  $n$  is greater than or equal to 325, or  $n$  is greater than or equal to 350; for one or more molecules or combinations of molecules yielding known sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal, providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  sensory receptors of the mammal; where  $n$  is

greater than or equal to 5,  $n$  is greater than or equal to 10,  $n$  is greater than or equal to 20,  $n$  is greater than or equal to 50,  $n$  is greater than or equal to 75,  $n$  is greater than or equal to 100,  $n$  is greater than or equal to 125,  $n$  is greater than or equal to 150,  $n$  is greater than or equal to 175,  $n$  is greater than or equal to 200,  $n$  is greater than or equal to 225,  $n$  is greater than or equal to 250,  $n$  is greater than or equal to 275,  $n$  is greater than or equal to 300,  $n$  is greater than or equal to 325, or  $n$  is greater than or equal to 350; for one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal by comparing the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal to the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal. The sensory receptors used in this method may include a receptor disclosed herein, or fragment or variant thereof. The maximum number of taste receptors that are needed to mimic the native repertoire (*e.g.*, about 50) may be less than the maximum number of olfactory receptors that are needed (*e.g.*, about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

Assaying for ligand-receptor binding in a large set of sensory receptors is envisioned to mimic the function of the nose or tongue in sensory perception of chemical sensants. For a set of sensory receptors with a redundancy of ligand-binding domains, the resultant signal is a summation of the interactions of all sensory receptors in the set: none, one, or a few of which have ligand-binding domains that are a perfect fit for the sensant; some of which have ligand-binding domains that are only an imperfect fit for the sensant; and most of which do not significantly bind to the sensant. The individual sensory receptor's binding affinity for sensant varies accordingly. Thus, a suitably large set of ligand-binding domains from sensory receptors will be analogous to any ability of the native repertoire of olfactory or taste receptors to tolerate varying degrees of mismatch between ligand and ligand-binding domain.

The complication of desensitization of sensory receptor signaling will also be avoided by using the invention instead of preparations of nasal or tongue epithelium containing native sensory receptors. For example, the event of binding between ligand and receptor can be separated from more complicated downstream signaling events in the epithelial cells. But the latter events can be reconstituted in the invention by transferring the sensory receptor of interest into appropriate host cells containing an intact and functional signaling pathway.

#### H. Administration of Novel Sensant Compositions

Sensory modulators can be administered directly to a mammal (*e.g.*, human) for modulation of sensory perception *in vivo*. Administration is by any of the routes normally used for introducing a modulator compound into ultimate contact with the tissue to be treated (*e.g.*, nose or tongue). The olfactory modulators are administered in any suitable manner, optionally with acceptable carriers. Suitable methods of administering such modulators are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route. Acceptable carriers are determined at least in part by the particular components of the composition to be administered (*e.g.*, stabilizing the sensants), as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed. 1985).

The sensory modulators, alone or in combination with other suitable components, can be made into aerosol formulations (*i.e.*, they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichloro-difluoromethane, propane, nitrogen, and the like that may or may not contribute to sensory perception. Other possible formulation include dry or liquid forms, powders or tablets, solutions of polar (*e.g.*, water) or nonpolar (*e.g.*, alcohol) solvents, emulsions or suspensions, creams, gels, lotions, and syrups.

Formulations suitable for administration include aqueous and non-aqueous solutions, isotonic sterile solutions, which can contain antioxidants; buffers,

bacteriostats, and solutes that render the formulation isotonic, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by orally, topically, intravenously, intraperitoneally, intravesically, or intrathecally. Optionally, the compositions are administered orally or nasally. The formulations of compounds can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials. Solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. The modulators can also be administered as part of a prepared drug, food, or cosmetic. In particular, an unpleasant odor or taste (*e.g.*, sulfur or bitter, respectively) may not be perceived as such and/or its effects reduced by blocking the binding between sensant ligand and sensory receptor by adding a competitor ligand that blocks binding between cognate ligand and receptor, or inhibiting or reducing signal transduction. In contrast, a pleasant odor or taste can be mimicked or enhanced. Primary sensants are preferred because the subset of activated cells is kept small and the effects limited to projection into a specific region of the brain. But novel olfactants or combinations thereof that bind only a few olfactory receptors (*e.g.*, having less than five different ligand-binding domains) would also be useful.

The dose administered to a mammal (*e.g.*, human) should be sufficient to effect a beneficial response in the subject over time. The dose will be determined by the efficacy of the particular sensory modulators employed and the condition of the subject, as well as the body weight or surface area of the area to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular compound or vector in a particular subject. In determining the effective amount of the modulator to be administered, a physician may evaluate circulating plasma levels of the sensory modulator, modulator toxicities, and the production of anti-modulator antibodies. In general, the dose equivalent of a modulator is from about 1 ng/kg to 10 mg/kg for the typical mammal. For administration, sensory modulators can be administered at a rate determined by the  $ED_{50}$  of the modulator, and the side-effects of the inhibitor at various concentrations, as applied to the mass and overall health of the mammal. Administration can be accomplished via single or divided doses.

## I. Kits

Sensory receptor genes, or fragments or variants thereof are useful tools for identifying cells expressing sensory receptors, for forensics and paternity determinations, and for examining signal transduction in isolated cells. Sensory receptor family member-specific reagents that specifically hybridize to sensory receptor nucleic acids, such as AOFLF1 probes and primers, and sensory receptor specific reagents that specifically bind to a sensory receptor protein, *e.g.*, anti-sensory receptor antibodies are used to examine expression in cells and regulation of signal transduction. For example, one or more family member-specific reagents may be used to detect poly-morphisms that are linked to genetic anosmia or to detect allelic exclusion.

Nucleic acid assays for the presence of DNA and RNA for a sensory receptor family member in a sample include numerous techniques are known to those skilled in the art, such as Southern analysis, Northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybridization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-250 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, a sensory receptor protein can be detected with the various immunoassay techniques described above. The test sample is typically compared to both a positive control (*e.g.*, a sample expressing a recombinant sensory receptor protein) and a negative control.

The present invention also provides for kits for screening for novel modulators of sensory receptor family members. Such kits can be prepared from readily available materials and reagents, as well as any of the aforementioned products. For example, such kits can comprise any one or more of the following materials: sensory receptor nucleic acids or proteins, reaction tubes, and instructions for testing sensory receptor activity. Optionally, the kit contains a biologically active sensory receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

## Examples

## AOLFR1 sequences:

MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVLFLGMYLVTVIGNGLIIVAISLD  
 TYLHTPMYFLANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLLGTM  
 5 AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIALTHTLILLIQLLFCNHNTLPHFCDLAPLL  
 KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGWKAFSTCGSHLTVVLLFY  
 GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMNPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID  
 NO: 1)  
 10 ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA  
 CCATCACTGAATTCATTCTCCTGGGATTTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT  
 GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA  
 TCAGCTTGGATACGTACCTTCATACCCCATGTATCTCTTCCTTGCCAATCTATCCTTTGCT  
 GATATTTCTCCATTTCCAACCTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC  
 15 AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCTCATT  
 GACAATTTGCTCTTGGGGACCATGGCCTATGACCACCTTTGTGGCGATCTGCCACCTCTGA  
 ATTATACAATTCTCATGCGGCCAGGTTGCGCATTTTGTCTCACAGTCATCTCATGGTTCCTC  
 AGTAATATTATTGCTCTGACACACACCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA  
 CACTCTCCACACTTCTTCTGTGACTTGGCCCTCTGCTCAAACCTGCTCTGTTAGATACAT  
 20 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCTTTACACTC  
 AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCTGAGAGTATCTTCCACACAGGGAA  
 AGTGGAAGCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC  
 CATTGTAGGCGTGTACTTTTCCCTCTCCACTCACCTGAGGACACTGATAAGATTGGT  
 GCTGTCTATTCACTGTGGTGACACCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA  
 25 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCTTTGA (SEQ  
 ID NO: 2)

## AOLFR2 sequences:

MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLMYVITVVGNLGMIIKINPKFHTPMYFFL  
 30 SHLSFVDFCYSSIVTPKLENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC  
 NPLLYTVAMSQRLLCALLVAGSYLWGMFGPLVLLCYALRLNFGPNVINHFFCEYALISVSGS  
 DILIPHLLLSFATFNEMCTLLILTSYVFIVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTLFL  
 YCVPSKNSRQTVKVASVFYTVVNPMLNPPFIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:  
 3)  
 35 ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCACCTTTGCCCTTTTAGGTTTCACAG  
 ATTACCAAAGCTTCAGATTCCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG  
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCCAAATTCACACTCCTATGT  
 ACTTTTCTTAGTCACCTCTCTTTTGTGATTTTGTGTTACTCTTCCATTGTCACTCCCAAGC  
 40 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA  
 CTTCTGTCTGCTGCTGTGGTGACAGAGTCTTTCTTGTGTCAGTGATGGCCTATGAC  
 CGCTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTCACAGAGGCTCTGTG  
 CCCTGCTGGTGGCTGGGTCATATCTCTGGGGCATGTTTGGCCCTTGGTACTCCTTTGTTAT  
 GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTTGTGAGTATACTGC  
 45 TCTCATCTCTGTGTCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTCAGCTTCGCCA  
 CCTTCAATGAGATGTGTACACTACTGATCATCCTCACTTCCTATGTTTTCATTTTGTGACT  
 GACTAAAAATCCGTTCTGTTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCCTCCCAAC  
 TGAATGCTATCACCATCTTCCATGGGACCATCCTTTTCTTTACTGTGTACCCAACTCCAAA  
 50 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTCTGGAAGTTAATACA  
 TACACAAGTTCCATTTCACTGA (SEQ ID NO: 4)

## AOLFR3 sequences:

MLLTDRNTSGTTFLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIVIIKINPKLHTPMYFFLSQ  
 55 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFCTFVVTESFLLAVMAYDRFVAICNPL  
 LYTVDMSQKLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHFFCEFSLLSLSCSDTYI



NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITFHGTILFLYCV  
PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

5 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT  
ACCCAGAACTGCAAGTCCCACTCTTCCTGGTTTTCTGGCCATCTACAATGTCAGTGTGCTA  
GGGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAAGTGCATACCCCATGTACT  
TTTTCTCAGCCAACTCTCCTTTGTGGATTCTGCTATTCTCCATCATTGCTCCCAAGATG  
TTGGTGAACCTTGTGTCAAAGACAGAACCATTTTCATTTTTAGGATGCGTAGTACAATTCT  
10 TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTTATTAGCTGTGATGGCCTATGACCGC  
TTCGTGGCCATTTGCAACCCTCTGCTCTACACAGTTGACATGTCCAGAACTCTGCGTGC  
TGCTGGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAACTGACGTGCTCTGC  
TTTAAAGTTATGTTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC  
TACTCTCCCTTTCTTGCTCTGATACTTACATCAACCAGTGGCTGCTATTCTTTCTTGCCACC  
TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT  
15 CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCACCTG  
ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTTTACTGTGTGCCAACTCCAAAAA  
CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGTATCCCATGTTGAAT  
CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC  
ACCAAAGTCTTCTTACTGA (SEQ ID NO: 6)

20

**AOLFR4 sequences:**

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS  
LLDVMFSSVVPKVVVDTLISKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY  
TIIMSPRVCCMLVGGAWVGGFMHAMIQLLFMYQIPFCGPNIIDHFICDLFQLLTLACTDTHILGL  
25 LVTLNSGMMCVAIFLILIASYTVILCSLSYSSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV  
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

30 ATGGAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC  
TGTGGAAAATATTTTTCTGCTGTGTTTCTTGTCATGTATGTAGCCACAGTGTGGAAAATCT  
ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTACCTATGTATTTTTTCTTA  
CCTTCTTGCCCTTTTGGATGTCATGTTCTCATCTGTCGTTGCCCCAAGGTGATTGTAGAC  
ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCAGCTGTTTGTGGAGC  
ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC  
CATCTGTAAGCCCCTGCACTACACGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA  
35 GGAGGGGCTTGGGTGGGGGGATTATGCACGCAATGATACAACTTCTTTCATGTATCAAA  
TACCCTTCTGTGGTCCTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA  
CTTGCCCTGCACGGACACCCACATCCTGGCCCTCTTAGTTACCCTCAACAGTGGGATGATGT  
GTGTGGCCATCTTTCTTATCTTAATTGCGTCTACACGGTCATCCTATGCTCCCTGAAGTCT  
TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCACCTCACGGTGGTTG  
40 TATTGTTCTTTGTCCCCTGTATTTTCTTGACATGAGGCCTGTGGTCACTACCCCATAGAC  
AAGGCAATGGCTGTGTGACACTCAATCATCACACCCATGTTAAATCCCTTGATCTATACAC  
TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG  
CTGGGAAATAA (SEQ ID NO: 8)

**AOLFR5 sequences:**

45 MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTLNLANLGMIALIQVSSRLHTPMYFFLSH  
LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL  
LYTVMMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVN  
ETLLFLVATLNE SVTIMILTSYLLLTILKMGSAEGRHKAFSTCASHLTAITVFHGTVLSIYCRP  
50 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

55 ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC  
CTGAGTTGAGAGTCTGCCTCTTCCTGCTGTTCTTCTCATCTATGGAGTCACGTTGTTAGCC  
AACCTGGGCATGATTGCACTGATTCAGGTCAGCTCTCGGCTCCACACCCCATGTACTTTT  
TCCTCAGCCACTTGTCCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG  
GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGAATTCTACT

TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCCTGCTGGCCGTGATGGCCTATGACCGCTTT  
 GTGGCCATCTGTAACCCCTTGTCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC  
 TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTTGTGCTTAGCTCTT  
 AGGATCCCCCTTCTATAGATCTAATGTGATTAACCACTTTTTCTGTGATCTACCTCCTGTCTT  
 5 AAGTCTTGCTTGCTCTGATATCACTGTGAATGAGACACTGCTGTTCTGGTGGCCACTTTG  
 AATGAGAGTGTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT  
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTCACA  
 GCTATCACTGTCTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCCAGTTCAGGCAATA  
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACTC  
 10 TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC  
 CAAAATTCACCTCTAG (SEQ ID NO: 10)

#### AOLFR6 sequences:

MMASERNQSSPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS  
 15 HLSTDFCFSTVVPKLLNLVVEYRTISFSGCIMQFCFACIFGVTETFMLAAMAYDRFVAVCK  
 PLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLDLDFCESTFINNFICDHSVIVSASYSPTYIS  
 QRLCFIIAIFNEVSSLIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTLFLYCVPNP  
 KTSSLIVTVASVFYTVAPMLNPLIYSLRNKDINNMFEKLVVTKLIYH (SEQ ID NO: 11)

20 ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG  
 AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTTTCGTCTACACAGTCACTGTA  
 GTGGGGAACCTGGGCATGATAATAATCATCAGACTCAATTCAAACCTCCATACAATCATGT  
 ACTTTTTCCTTAGTCACTTGTCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA  
 CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTCTGTTGTCATGCAAT  
 25 TTTGTTTTGCTTGCATTTTTGGAGTGACAGAACTTTCATGTTAGCAGCATGGCTTATGAC  
 CGTTTTGTGGCAGTTTGTAAACCCCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC  
 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT  
 CTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT  
 AATTGTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA  
 30 TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC  
 ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC  
 TGACAGCCATCACTATCTTCCATGGAACATCCTTTTCTTTACTGTGTTCTTAATCCTAAA  
 ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA  
 ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT  
 35 CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

#### AOLFR7 sequences:

MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRKSRSRDMEIKNYSSSTSGFILLGLSSNPQLQKPLF  
 AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISY  
 40 VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLMLLGSCSISHLHSL  
 FRVLLMSRLSFCASHIIKHFFCDTQPVLKLSGSDTSSSQMVVMTETLAVIVTPFLCIIFSILRMV  
 TVLRIPSAAGKWKAFTSCGSHLTAVALFYGSIHYVYFRPLSMYSVVRDRVATVMYTVVTPMLN  
 PFIYSLRNKDMKRGLKKLQDRIYR (SEQ ID NO: 13)

45 ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA  
 CATCTCTCCCACTGCTTCTCCAAACCCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA  
 CTACAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCAACCCTCAGCTGCAG  
 AAACCTCTCTTTGCCATCTTCCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT  
 CATCCCGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACTTTTTCTCAGCAACT  
 50 TGTCTTTCATGGATATCTGCTTCAACAGTCATAGTGCTAAGATGCTGGTGAATTTCTA  
 TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTTATGGCAT  
 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG  
 CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT  
 TCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT  
 55 CTGTGCCTCTCACATCATTAAAGCACTTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT  
 GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCAATTGTGAC

5 CCCCTTCCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCCT  
CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCTCACTGCAGTAGCCCT  
TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTA CTAGTGGTTAGGG  
ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTTCATCTACAG  
CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA  
A (SEQ ID NO: 14)

**AOLFR8 sequences:**

10 MATSNHSSGAEFILAGLTQRPELQLPLFLLFLGIYVVTVVGNLGMIFLIALSSQLYPPVYYFLSH  
LSFIDLCYSSVITPKMLVNFVPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPPLY  
NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI  
LLFIIGGVNTLATTALVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMFKPPSS  
TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

15 ATGGCTACTTCAAACCATTCCTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC  
CAGAACTTCAACTGCCACTCTTCCTCCTGTTCTTGGGAATATATGTGGTCACAGTGGTGGG  
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCTCCAGTGTATTATT  
TTCTCAGTCATTTGTCTTTCATTGATCTCTGCTACTCCTCTGTCAATTACCCCTAAGATGCTG  
GTGAACCTTGTTCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT  
20 CTTCTTATTTTTGTAAATGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT  
GTTGCTATCTGTCGCCCACTGCTTTACAATATTGTCAATGTCCACAGGGTCTGTTCCATAAT  
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA  
GTGTTGTCACTCTGTAGGTCTCATACGGTCAGTCATTATTTTGTGATATTCTCCCTTATT  
GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTCAATTATTGGAGGAGTT  
25 AATACCTTAGCAACTACACTGGCGGTCTTATCTCTTATGCTTTTCATTTTCTCTAGTATCCT  
TGGTATTCACTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTGTAGCTCCCATCTCTTG  
GCTGTGGGCATCTTTTTTGGGTCTATAACATTCATGTATITCAAGCCCCCTTCCAGCACTAC  
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT  
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA  
30 AGGCAGTCATCCTGA (SEQ ID NO: 16)

**AOLFR9 sequences:**

35 MLARNNSLVTEFILAGLTDRPEFWQFFFLFLVIYIVTMVGNLGLITLFLNSHLHTPMYYFLFN  
LSFIDLCYSSVFTPKMLMNFVSKKNISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL  
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHLYCDILPLLQLSCTSTYV  
NEVVVLIVVGITNITVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY  
SSGSMEQKGKVSFVYTNVVPMLNPLIYSLRNKDVKVALRKALIKJQRNIF (SEQ ID NO: 17)

40 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC  
CAGAGTTCTGGCAACCTTCTTTTTCTGTTCTAGTGATCTACATTGTCACCATGGTAGGC  
AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACCAATGTACTATTT  
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT  
GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC  
TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT  
45 GGCCATCTGTAATCCATTGCTGTATAAGGTACCATGTCCCATCAGGTCTGTTCTATGCTCA  
CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAG  
ACTCACCTTCTGCAGTGCTAATATCATTAAACCATTACTTGTGTGACATACTCCCCCTCCTCC  
AGCTTTCCTGCACCGACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA  
TATCACGGTACCCAGTTGTACCATCTCATTTCTTATGTTTTTCAATTGCTACTAGCATTCTTC  
50 ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGC  
TCTGTCTCTGTTTTTGGGTGAGCGGCATTGATGTATATTAAATATTCTTCTGGATCTATGG  
AGCAGGGAAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCCTCATC  
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAATTCAG  
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

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**AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFNL  
 SFIDLCYSSVFTPKMLMNFVSKKNIISYVGCMTQLFFFLFFVISECYILTSMA YDRYVAICNPPLY  
 KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMLRLTFCSANIINHLYCDILPLLQLSCTSTYVN  
 5 EVVVLIVVGINIMVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS  
 SGSMEQGVVSSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC  
 CAGAGTTCCGGCAACCCCTCTTTTCTGTTTCTAGTGATCTACATTGTCACCATGGTAGGC  
 10 AACCTTGGCTTGATCATTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT  
 CCTCTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT  
 GAACTTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTTCT  
 TTCTCTTTTTTGTATCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG  
 GCCATCTGTAATCCATTGCTGTATAAGGTCAACCATGTCCCATCAGGTCTGTTCTATGCTCAC  
 15 TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGCTTAGA  
 CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA  
 GCTTTCTGCACCGCTAATATCATCAACGAGGTGGTGTGTTCTCATTGTTGTGGGTATTAAT  
 ATCATGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTATTGTCACCTAGCATTCITCA  
 TATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCATTGCT  
 20 CTGTCTCTGTTTTTGGGTGAGCGGCATTGATGATATTAATATTCTTCTGGATCTATGGA  
 GCAGGGAAAAGTTTCTTCTGTTTTCTACATAATGTGGTGCCCATGCTCAATCCTCTCATCT  
 ACAGTTTGAGGAACAAGGATGTCAAAGTGTCACTGAGGAAAGCTCTGATTAAAATTCAGA  
 GAAGAAATATATTCTAA (SEQ ID NO: 20)

**AOLFR11 sequences:**

MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGNPSLHTPMYFFLFNL  
 FIDLCYSCVFTPKMLNDFVSESIISYVGCMTQLFFFCFFVNSECYVLVSMAYDRYVAICNPPLY  
 MVTMSPRVCFLLMFGSYVVGFAAGAMAHTGSMRLRLTFCDNSVIDHYLCDVLPPLLQLSCTSTHV  
 30 SELVFFIVVGVITMLSSISIVISYALILSIPSAEGRSKAFSTWGSIIAVALFFGSGTFTYLTTS  
 FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTTGGGATTATCAGAACAGC  
 CAGAGCTCCAGCTCCCTCTTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC  
 AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCATGTACTTTTT  
 35 CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTECTGTGTGTTACCCCCAAAATGCTGA  
 ATGACTTTGTTTCAGAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTTCTTC  
 TGTTTCTTTGTCAATTCTGAGTGCTATGTTGGTATCAATGGCCTATGATCGCTATGTGGC  
 CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCAAGGGTCTGCTTCTGCTGATGT  
 TTGGTTCCTATGTGGTAGGGTTTGGTGGGGCCATGGCCACACTGGAAGCATGCTGCGACT  
 40 GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGACGC  
 TCTCCTGCACACAGCACCCATGTCAGTGAGCTGGTATTTTTCATTGTTGTTGGAGTAATCACC  
 ATGCTATCCAGCATAAGCATCGTCATCTCTTACGCTTTGATACTCTCCAACATCCTCTGTAT  
 TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCACATGGGGCTCCACATAATTGCTGTT  
 GCTCTGTTTTTTGGGTGAGGGACATTCACCTACTTAACAACATCTTTTCTGGCTCTATGAA  
 45 CCATGGCAGATTTGCCTCAGTCTTTTACACCAATGTGGTTCCTCATTAACCTTCGATCT  
 ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCTGAAGAGAGTGCTCT  
 TCTAA (SEQ ID NO: 22)

**AOLFR12 sequences:**

MERNHNPDNCNVLNFFADKKNKRRNFGQIVSDVGRICYSVLSLGEPTTMGRNNLTRPSEFIL  
 LGLSSRPEDQKPLFAVFLPIYLITVIGNLLIILAIRSDTRLQTPMYFFLSILSFVDICYVTVIIPKMLV  
 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMADRYVAICNPFHYITIMSHRCCVLLLVLS  
 FCIPHFHSLHLLTNQLIFCASNVIIHFFCDDQPVKLKSCSSHVKEITVMTEGLAVIMTPFSCIII  
 SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP  
 55 MLNPFYSLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTCTTTGCTGATAAGA  
 AGAATAAAAGGAGAAATTTTGGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG  
 TTAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAAGACCCTCTGA  
 ATTCATCCTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC  
 5 TCCCCATCTACCTTATCACAGTGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA  
 CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTTGTGACATTTGCT  
 ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC  
 TTACGGTGAGTGTCTGACCCAGATGTACTTTTTCTTAGCCTTTGGAACACAGACAGTTAC  
 CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA  
 10 CCATTATGAGTCACAGATGCTGTGTCCTGCTTCTGGTCTCTCCTTCTGCATTCCACATTTT  
 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA  
 TCATTTTTCTGCGATGATCAACCAGTGCTAAAATTGTCCTGTTCCCTCCCATTTTGTCAAAG  
 AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTTCATGCATCATCAT  
 CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCTTCAGCTGCTGGAAAGCGTAAA  
 15 GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCTGTTTTATGGAAGCATTAGCTA  
 TGTCTATTTTCAGCCCCTGTCCAATACTGTCAAGGATCAAAATAGCAACAATTATCTAC  
 ACCGTAAGTACTGCTTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC  
 AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

20 **AOLFR13 sequences:**

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFTLLGNKTHIVLSHLDPHLHNP MYFFFSNL  
 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL  
 HYTVVMHPCLYVLMASWSVIGFANSLLQTVLILLTL CGRNKLEHFLCEVPPLKLACVDTT  
 MNESEFFVSVIII LPVALIIFSYSQIVRAVVRIKSATGQRKVFGTCGSHLTVVSLFYGTAIYAY  
 25 LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:  
 25)

ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC  
 CTCAGCTGGAGCTAGTCCTCTTTGTGGTTCTTTTGATCTTCTATATCTTCACTTTGCTGGGG  
 30 AACAAAACCATCATTGTATTATCTCACTTGGACCCACATCTTACAATCCTATGTATTTTTT  
 TTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG  
 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAGCTGTACAT  
 CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT  
 GCAGCTGTTTGCAGGCCCCCTCCACTACACAGTAGTCATGCACCCTGTCTGTATGTGCTGA  
 35 TGGCTTCTACTTCATGGGTCAATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG  
 CTTTAAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCCCTCCATTGCT  
 CAAGCTTGCTGTGTTGACACTACTATGAATGAATCTGAACCTTCTTTGTGAGTGTCATTA  
 TTCTTCTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTCAGGGCAGTCGTG  
 AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTTTGGGACATGTGGCTCCCACTCACA  
 40 GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCCGGCAACAATACTC  
 TCAGGATCAGGGCAAGKTCATCTCTCTTCTACACCATCATTACCCCATGATCAACCCC  
 CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG  
 AACTACGACTCCAGATGA (SEQ ID NO: 26)

45 **AOLFR14 sequences:**

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL  
 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSSAIGPKMLVDLLPRATIPYTACALQMF  
 VFAGLADTECLLAAMAYDRYVAIRNPLLYTTAMSQRCLALLGASGLGGAVSAFVHTTLTF  
 RLSFCRSRKINSFFCDIPPLLAISCDTSLNELLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE  
 50 GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALDTDKMASVFYTLVIPSLNPLIYSLRNKE  
 VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG  
 GATGAACTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTCGTCCTCCTGGGC  
 55 ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTCCTGACCTGCCTGCCTGTCTACCTGG  
 TGAGCCTGCTGGGAAACATGGGCATGGCGTGTGATCCGCATGGATGCCCGGCTCCACA

CACCTATGTACTTCTTCTGGCCAACCTCTCCCTGCTGGATGCCTGCTATTCCTCCGCCATC  
 GGGCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG  
 CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTGCTTGTGTCAGCCAT  
 GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATAACAACAGCTATGTCGCAG  
 5 CGTCTATGCCTGGCCTTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTT  
 ACACAACCCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG  
 CGATATCCCTCCACTGCTGGCCATCTCGTGCAGTGACACCAGTCTCAATGAACTCCTTCTCT  
 TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTTAGCTATCACGGTGTCTTATGGCTT  
 CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGCGAGGGCAGTCGGCGAGCAGCCTCCAC  
 10 CGGTGGTTCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG  
 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG  
 TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT  
 CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCAGTGA (SEQ ID NO: 28)

15 **AOLFR15 sequences:**

MRENNQSSTLEFILLGVTGQQEQEDFFYLFLFIYPITLIGNLLIVLAICSDVRLHNPMPYFLLANLS  
 LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYILAAMAYDRAVAISHPLH  
 YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLKLSCSDIHFHV  
 KMMYLGVGIFSVPLLCIVSYIRVFSTVFQVPSTKGVLKAFSTCGSHLTVVSLLYYGTVMGTYFR  
 20 PLTNYSLKDAVITVMYTAVTPMLNPFYISLRNDRMKAALRKLFNKRIS (SEQ ID NO: 29)

ATGAGGGAAAATAACCAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC  
 AGGAACAGGAAGATTTCTTCTACATCCTCTTCTGTTCAATTAACCCATCACATTGATTGGA  
 AACCTGCTCATTGTCCTAGCCATTTGCTCTGATGTTGCGCTTCACAACCCCATGTATTTTCT  
 25 CCTTGCCAACCTCTCCTTGGTTGACATCTTCTCTCATCGGTAACCATCCCTAAGATGCTGG  
 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT  
 CATGATAGCCTTGGGTAACACAGACAGCTATATTTTGGCTGCAATGGCATATGATCGAGCT  
 GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC  
 TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCACACTCTGCTCACAGC  
 30 TAGTCTGTCTTCTGTGGCAACCAGGAAGTGGCCAACTTCTACTGTGACATTACCCCTTG  
 CTGAAGTTATCCTGTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA  
 TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTGAGTCTTCTCCACAGTCTTCC  
 AGGTTCTTCCACCAAGGGCGTGCTCAAGGCCCTTCTCCACCTGTGGTTCACCTCACGGT  
 TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTTGACCAATTATAGCC  
 35 TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTCAT  
 CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT  
 CTCCTCGTAA (SEQ ID NO: 30)

**AOLFR16 sequences:**

40 MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMTVAGNLGMIVLIQANAWLHMPMPYFFLSH  
 LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLQCYLFIALVHVEIYILAVMAFDYMAICNPLL  
 YGSRMSKSVCSFLITVPYVYGALTGLMETMWTYNLAFCGPNEINHFCADPPLIKLACSDTYN  
 KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR  
 PPSKESVEQGMVAVFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

45 ATGAGAAGAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG  
 GAATTACAAATTCTCCTCTTACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA  
 ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTTC  
 CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG  
 50 AGATTTTCTTTTTCAGAGAAGAAAAGCATTTCCTATCCTGCCTGTCTTGTGAGTGTACCTT  
 TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTGTACCGGTACAT  
 GGCCATCTGCAACCCTCTGCTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCTCCTC  
 ATCACGGTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA  
 ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT  
 55 TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG  
 AACCTTTCTTTTCTCTTCTCATCATATGATTTTCTTACCTTTACATTTTCTCCTGCTATTTTA



AAGATTGCTCTACAGAGGGCAGGCAAAAAGCTTTTTCTACCTGTGGCTCCCATCTGACAG  
 CTGTCACTATATTCTATGCAACCCCTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT  
 GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA  
 TAATTTATAGCCTTAGAAATAAAAATGTAAAAGAAGCATTAAATCAAAGAGCTGTCAATGA  
 5 AGATATACTTTTCTTAA (SEQ ID NO: 32)

**AOLFR17 sequences:**

MLNFTDVTEFILLGLTSRREWQVLFHIFLVVYIITMVGNI GMMVLIKVSPQLNNPMYFFLSHL  
 FVDVWFSSNVTPKMLENLFSDKKTITYAGCLVQCFFIALVHVEIFILAAMAFDRYMAIGNPLL  
 10 YGSKMSRVVCIRLITFPYIYGFLTSLAATLWTYGLYFCGKIEINHFYCADPPLIKMACAGTFVKE  
 YTMILAGINFTYSLTVIISYLFILAILRMRSAGEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRPTE  
 ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT  
 15 GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC  
 GGCATGATGGTGTTAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTCTCTCA  
 GTCATTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAC  
 CTGTTTTAGATAAAAAACAATTAATGCTGGTTGTTAGTACAGTGTCTTCTTCTCAT  
 TGCTCTGTCCATGTGGAATTTTATTCTTGTGCGATGGCCTTTGATAGATACATGGCAA  
 20 TTGGGAATCCTCTGCTTTATGGCAGTAAAATGTCAAGGGTTGTCTGTATTGACTGATTAC  
 TTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT  
 ACTTCTGTGGAATAATTGAGATCAACATTTCTACTGTGCAGATCCACCTCTCATCAAAAT  
 GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACTTC  
 ACATATTCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT  
 25 GCGCTCAGCAGAAGGAAGGCAGAGGCCTTTCCACATGTGGGTCCCATCTGACAGCTGT  
 CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG  
 GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA  
 TCTACAGTCTGAGGAACAAGGATGTGAAAAGGCCATGATGAAAGTGATCAGCAGATCAT  
 GTTAA (SEQ ID NO: 34)

30

**AOLFR18 sequences:**

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVVYLVTLLGNLGMIMLMRLDSRLHTPMYFFLT  
 NLAFLVLCYTSNATPQMSTNIVSEKTI SFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP  
 LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK  
 35 EHAMFISAGFNLSSSLTIVLVSYAFILAAILRIKSAEGRHKAFTSTCGSHMMAVTLFYGTLFCMYI  
 RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC  
 CGGAACCTCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTTGTTTACCTCGTCACCCCTGCTAGGC  
 40 AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT  
 TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC  
 GACTAATATCGTATCTGAGAAGACCATTTCTTGTGCTGGTTGCTTTACACAGTGCTACATTT  
 TCATTGCCCTTCTACTACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT  
 GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG  
 45 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCCTGACCTCCG  
 CCTGACCTTCTGTAGATCCAATGTCATCAACCACTTCTACTGTGCTGACCCGCCGCTCATT  
 AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTCATATCTGCTGGCTTCAAC  
 CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCTATGCCTTCATTCTTGTGCCATCCTCCG  
 GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC  
 50 GTTGAGGAATCTAAAATAATAGCTGTCTTTACACCTTTGTGAGTCCGGTACTTAATCCAT  
 TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCTGAGATGA  
 (SEQ ID NO: 36)

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**AOLFR19 sequences:**

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLILAIYSDPRLHTPMYFFLSNL  
 SFMDICFTTVIVPKMLVNFLETKIISYVVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH  
 YDVVMKPWHCLLMMLGSCSISHLHSLFRVLLMSRSLFCASHIHKHFFCDTQPVLKLSGSDTSSSQ  
 5 MVVMTETLAVIVTPFLCTIFSYLQIIVTVLRIPSAAGKWKAFTSCGSHLTVVVLFYGSVIYVYFR  
 PLSMYSVMKGRVATVMYTVVTPMLNPFYISLRNKDMKRGLKCLRHRIS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA  
 ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCCTCATCATGTACCTACTCACTGCGGTG  
 10 GGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT  
 TTTTCTCAGCAACTTGTCTTTTATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATG  
 CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT  
 ACTTCTTCATGGCATTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG  
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA  
 15 CTCATGCTATTGGGTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTAT  
 GTCTCGCTTGTCTTTCTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTG  
 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT  
 AGCTGTCATTGTGACCCCTTCTGTGTACCATCTTCTCCTACCTGCAAAATCATCGTCACTG  
 TGCTCAGAATCCCTCTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCT  
 20 CACTGTAGTGGTCTGTCTATGGGAGTGTCATCTATGTCTATTTTAGGCCTCTGTCCATGT  
 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA  
 ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC  
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

**AOLFR20 sequences:**

MVEENHTMKNEFILTGFTDHPKLTLLFVVFVFAIYLITVVGNI SLVALIFTHCRLHTPMYIFLGN  
 LALVDSCCAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP  
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFCYCDTLPLYRLSCVDPF  
 INELVLFIFSGSVQVFTIGSVLISYL ILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP  
 30 NLEEGGNDIPAAILFTIVVPLNPFYISLRNKEVISVLRKILLKIKSQGSVNK (SEQ ID NO: 39)

ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC  
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCGTGGTGGG  
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTGCGCTTCACACACCAATGTACATC  
 35 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGTGTGCCTGTGCTATTACCCCCAAAATGTT  
 AGAGAACCTCTTTTCTGAGGGCAAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT  
 TTTCTTTGCACTGTGGAACCTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT  
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA  
 GATGACCACAGGCGCCTTCATAGCTGGAAATCTGCATTCCATGATTATGTAGGGCTTGTA  
 40 TTTAGGTTAGTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT  
 GTATAGACTCTCCTGTGTGACCCCTTCATCAATGAACTGGTTCTATTCTATCTTCTCAGGTT  
 CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTACTATT  
 TTCAGAAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTGTGCATCCCACTTTT  
 CATCAGTTTCATTATTCTATGGATCTATTTTTTCTATACATTAGACCAAATTTGCTTGAA  
 45 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTTACAATAGTAGTTCCCTTACTAAATC  
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTCTGCTGAA  
 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

**AOLFR21 sequences:**

MEPRKNVTDVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTVSETLGSPPMSFFLAGL  
 TFIDIIYSSSISPRLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMA YDRYVAICKPLHYLV  
 IMRQWVCVLLLVVSWVGGFLQSVFQLSIYGLPFCGPNVIDHFFCDMPYLLKLACTDTHVIGLL  
 VVANGGLSCTIAFLLLLISYGVILHSLKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR  
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

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TCACCCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG  
 CTGAAGCTTGCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT  
 TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCCTATCTGCTCATCATCAAGACCATT  
 TTGAAAGTGAAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA  
 5 CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA  
 TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC  
 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA  
 GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

10 **AOLFR25 sequences:**

METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITTVMGNILIITVTSDSQLHTPMYFLLRN  
 LAVLDLCFSSVTAPKMLVDLLSEKKTISYQGC MGQIFFHFLGGAMVFFLSVMAFDRLIAISRPL  
 RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVLR LACTDT  
 SLLEFLKISNSGLLDVVWFFLLMSYLFILVMLRSHPGEARRKAASTCTTHIIVSMIFVPSIYLY  
 15 ARPFTFPMDKLV SIGHTVMTPLNPMIYTLRNQDMQAAVRRLGRHLV (SEQ ID NO: 47)

ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCTCTGGGGCTCTCGCAGACTC  
 GGGAGCTCCAGCGTTTCTGTTTCTAATGTTTCTGTTTGTCTACATCACCCTGTTATGGGA  
 AACATCCTTATCATCATCACAGTGACCTCTGATTCCCAGCTCCACACACCCATGTACTTTCT  
 20 GCTCCGAAACCTGGCTGTCTAGACCTCTGTTTCTTCTCAGTCACTGCTCCAAAATGCTAG  
 TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT  
 CTTCCACTTTTTGGGAGGTGCCATGGTCTTCTTCTCAGTGATGGCCTTTGACCGCCTCA  
 TTGCCATCTCCCGCCCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGGCT  
 GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC  
 25 CCACTGCCCTTCTGTGGCCCAACATTTTGGATAACTTCTACTGTGATGTTCCCAAGTACT  
 GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG  
 CTGGATGCTGCTGGTTCTTCTCCTCCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG  
 GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCACCCACATCATCGT  
 GGTTCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA  
 30 TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCATGCTCAACCCCATGATCTA  
 TACCCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT  
 TTGA (SEQ ID NO: 48)

**AOLFR26 sequences:**

MAAKNSSVTEFILEGLTHQPGLRIPLFFFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS  
 35 LIDFCFSTTTTPKMLMSFVSRKNIISFTGCMTQLFFFCFFVSESFILSAMAYDRYVAICNPLLYT  
 VTMSQVCLLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILP LLELSCNSSYMN  
 ELVVFIVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP  
 LSILPLEQGVSSLFYTHIVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG  
 GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA  
 CCTGGGCTTGATAACCCTGATTGGGCTGAACTCTCACCTGCACACTCCCATGTACTTCTTCC  
 TTTTAACTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG  
 45 AGTTTTGTCTCAAGGAAGAACATATTTCTTTCACAGGGTGTATGACTCAGCTCTTCTTCTT  
 CTGCTTCTTTGTCGTCTCTGAGTCCTTCATCCTGTGACGATGGCGTATGACCGCTACGTGG  
 CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTGCTCCTTTTG  
 TTGGGTGCCTATGGGATGGGGTTTGTGTTGGGCCATGGCCACACAGGAAGCATAATGAAC  
 CTGACCTTCTGTGCTGACAACCTTGTCATCATTTTCATGTGTGACATCCTTCTCTCCTTGA  
 50 GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC  
 GTTGGAATGCCCATTGTCACTGTCTTTATTTCTTATGCCCTCATCCTCTCCAGCATTCTACA  
 CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAAGTCCCACATAATTGTA  
 GTTTCTCTTTTCTTTGGTTCTGGTGCTTTTCATGTATCTCAAACCCCTTTCCATCCTGCCCTC  
 GAGCAAGGGAAGTGTCTCCCTGTTCTATACCATAATAGTCCCCGTGTTAAACCCATTAA  
 55 TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA  
 TCTTTTCTTAA (SEQ ID NO: 50)

**AOLFR27 sequences:**

- MPSQNYSIIEFNLFGFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATWIEHRLHTPMYFLFCTL  
SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR  
5 YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFCGSNVIHHFFCHVLSLLKLACENKT  
SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHYSFASFIY  
LKP KGLHSMYS DALMATTYTVFTPFLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:  
51)
- 10 ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC  
CCAGCACCTCCTGCCCATCTTGTTCTGTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG  
GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCCATGTACCT  
CTTCTGTGCACCCTCTCCGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC  
TGGCTGATCTGCTTTCCACCCATCATTCCATCACCTTTGTGGCTTGTGCCAACCCAGATGTTCT  
15 TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCTCTCTCTGGTCATGGGCTATGATCGCTA  
TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCGTGACTGTGCCCAT  
CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT  
TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTTTTTCTGTGTCATGTGCTTTCCCTCT  
TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTCATCATGGGTGTGATGCTGGTGTGTGT  
20 CACAGCCCTGATAGGCTGTTTATTCCTCATCATCTCTCTCTATGTCTTCATTGTGGCTGCCA  
TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTTTCTACGTGTGTATCCCACCT  
CACTGTGGTGGTCACGCACTATAGTTTGCCTCCTTTATCTACCTCAAGCCCAAGGGCCTCC  
ATTCTATGTACAGTGACGCCTTGATGGCCACCACCTATACTGTCTTACCCCCCTTCTTAGC  
CCAATCATTTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACTTTTACA  
25 GAAAATTCTGTCTCCAAGTTCTCTGA (SEQ ID NO: 52)

**AOLFR28 sequences:**

- MPNFTDVTEFTLLGLTCRQELQVLFFVFLAVYMITLLGNIGMIILISISPQLQSPMYFFLSHLSE  
ADVCSSNVTPKMLENLLSEKTI SYVGLVQCYFFIAVHVVEVYILAVMAFD RYMAGCXPLL  
30 YGSKMSRTVCVRLISVXYXYGFSVSLICTLWTYGLYFCGNFEINH FYCADPPLIQIACGRVHIKE  
ITMIVIAGINFTYSLSVVLISYTLIVVAVLRMR SADGRRKAFSTCGSHLTAVSMFYGTPIFMYLR  
RPTEESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)

- ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCGTCAGGAGC  
35 TACAGGTTCTCTTTTTGTGGTGTTCCTAGCGGTTTACATGATCACTCTGTTGGGAAATATT  
GGTATGATCATTTTGTATTAGCATCAGTCCTCAGCTTACAGAGTCCCATGTACTTTTCTCTGAG  
TCATCTGTCTTTTGGCGACGTGTGCTTCTCTCCAACGTTACCCCCAAAATGCTGGAAAAT  
TATTATCAGAGACAAAAACCATTTCTATGTGGGATGCTTGGTGCAGTGCTACTTTTTTCAT  
TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC  
40 GGCTGCAANCTCTGCTTTATGGCAGTAAAATGTCTAGGACTGTGTGTGTTCCGGCTCATCT  
CTGTGNNNTATGNNNTATGGATTCTCTGTGACGCTAATATGCACACTATGGACTTATGGCTT  
ATACTTCTGTGGAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA  
TTGCCTGTGGGAGAGTGCACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACCT  
CACATATTCCCTCTCGGTGGTCTCTCTCTACACTCTCATTGTAGTAGCTGTGCTACGCA  
45 TGCGCTCTGCCGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCCACTTGACGGCTGT  
TTCTATGTTTTATGGGACCCCCATCTTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA  
GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA  
TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT  
ATGTGAGGCAGTAA (SEQ ID NO: 54)

50

**AOLFR29 sequences:**

- MMSFAPNASHSPVFLLLGFSRANISYTLFFLFLAIYLTTLGNVTLVLLISWDSRLHSPMYYYLLR  
GLSVIDMGLSTVTLPQLLAHLVSHYPTIPAARCLAQFFFFYAFGVDTLVIAVMALDRYVAICD  
PLHYALVMNHQRCACLLALS WVVSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLLR  
55 ASCSDIHSNELAIFFE GFLMLGPCALIVLSYVRIGAAILRLPSAAGRRAVSTCGSHLTMVGFL

TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC  
 ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT  
 CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA  
 TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT  
 5 TAGTGGGCATGTCCTACCTGGGTGGATGTGTGAATGCTTGGACATTCAATTGGCTGCTTATT  
 AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTACCACTTT  
 TGAAGCTTGCTTGTTCCCATGATTTTACTTTTGAATAAATTCCAGCTATCTCTTCTGGATCT  
 ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATACCATCCT  
 GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT  
 10 GCAGTCACTCTGTTCTATGGGACCATACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC  
 AACTGACCAGAACAAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC  
 CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA  
 AAAATATTTTCTTGA (SEQ ID NO: 60)

15 **AOLFR32 sequences:**

MNSLKDGNHTALTGFILLGLTDDPILRVILFMILSGNLSIIILIRISSQLHHPMYFFLSHLAFADM  
 AYSSSVTPNMLVNFLVERNVSYLGCALQLSAFAFFATVECVLLAAMAYDRFVAICSPLLYSTK  
 MSTQVSVQLLLVVYIAGFLIAVSYYTSFYLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVLSF  
 SSGSIIVTVCVIAVCYIYLITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST  
 20 DQNKVSVVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNIT (SEQ ID  
 NO: 61)

ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA  
 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA  
 25 ATTATTCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGATTTCTTTCTGAGCCACTT  
 GGCTTTTGCTGACATGGCCTATTCATCTTCTGTCACACCCAACATGCTTGTAACCTTCCTGG  
 TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT  
 TGCAACAGTGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTGTGGCAATTTGC  
 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG  
 30 TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCTTCTATTTTTACTCTTCT  
 GTGGACCAAAATCAAGTCAATCAATTTTTCTGTGATTTTCGCTCCCTTACTTGAACCTCTCCTGT  
 TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTTCTTCTGGATCCATCATTGTGGTCAC  
 TGTGTGTGTCATAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA  
 CTGAGGGGGCACCACAAGGCCTTCTCCACCTGCACTTCCCACCTCACTGTGGTTACCCTGTT  
 35 CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC  
 AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC  
 TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACITTTCTC  
 ATGATGCTTGTTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

40 **AOLFR34 sequences:**

MLEGVEHLLLLLLLLTDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVITYLLTVSGNG  
 LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHLGCT  
 ECFLYTLMAFYDRFLAICKPLHYATIMTHRVNSLALGTWLGGTIHSFQTSFVRLPFCGPNRV  
 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRRNAFST  
 45 CAAHLTVVIVYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLLNSIYTLCKNEMKAALQRLGG  
 HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG  
 AACTGCAAAGTGGAACCAAGACTTCTGTGTCTCACTTCATTTTGGTGGGCCTGCACCACCC  
 50 ACCACAGCTGGGAGCGCACTCTTCTTAGCTTTCTTGTGCTATCTCCTCACTGTTTCTG  
 GAAATGGGCTCATCCTCACTGTCTTAGTGACATCCGGCTCCATCGTCCCATGTGCTT  
 GTTCTGTGTCACCTCTCCTTCTTGACATGACCAATTTCTTGTGCTATTGTCCCAAGATGC  
 TGGCTGGCTTTCTTGGGTAGTAGGATTATCTCCTTTGGGGGCTGTGTAATCCAACATTTT  
 TCTTCCATTTCTGGGCTGTACTGAGTGCTTCTTTACACACTCATGGCTTATGACCGTTT  
 55 CCTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC  
 TGGCTTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTTCCAAACAAGTTTGTATT

CCGGCTGCCCTTCTGTGGCCCCAATCGGGTCGACTACATCTTCTGTGACATTCTGCCATGC  
 TGGCTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTGCAGACATTGGCTT  
 CCTGGCCCTCACCTGCTTCATGCTCATCTCACTTCTATGGCTATATTGTAGCTGCCATCC  
 TGCGAATTCGTCAGCAGATGGGCGCCGAATGCCTTCTCCACTTGTGCTGCCACCTCAC  
 5 TGTTGTCAATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTCACAGGAGC  
 CCCTGGATGGGGTGGTAGCTGTCTTTTACACTGTCACTCCCTTGCTTAACTCCATCATC  
 TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA  
 GTGCAGCCTCACTGA (SEQ ID NO: 64)

10 **AOLFR35 sequences:**

MEPLNRTEVSEFFLKGFSGYPALHLLFPLCSAMYLVTLLGNTAIMAVSVLDIHLHTPVYFFLG  
 NLSTLDICYTPTFVPLMLVHLLSSRKTISFAVCAIQMCLSLSTGSTECLLAITAYDRYLAICQPL  
 RYHVLMSHRLCVLLMGAAWVLCCLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT  
 SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCCAFSTCLAHLAVLLFYGTIIFMY  
 15 LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO:  
 65)

ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC  
 CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCCCTCCTGGG  
 20 GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCCGTGTACTTC  
 TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCACCTTTGTGCTCTGATGCT  
 GGTCCACCTCCTGTCACTCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC  
 TGAGCCTGTCCACGGGCTCCACGGAGTGCTGCTACTGGCCATCACGGCCTATGACCGCTA  
 CCTGGCCATCTGCCAGCCACTCAGGTACCATGCTGCTCATGAGCCACCGGCTCTGCGTGCTG  
 25 CTGATGGGAGCTGCCTGGGTCTCTGCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA  
 TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACCTTCACTGCAAGATCCTGGCAGT  
 GCTGAAGCTGGCATGCGGCAACACGTGCGTCAGCGAAGACTTCTGCTGGCGGGCTCCAT  
 CCTGCTGCTGCCTGTACCCCTGGCATTCTGCTGCTCCTACTTGCTCATCTGCGCCACCA  
 TCCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAGCCTTCTCCACCTGCTTGGCACACCT  
 30 GGCTGATGTGCTGCTTTTCTACGGCACCATCATCTTCATGTACTTGAAGCCCAAGAGTAAG  
 GAAGCCACATCTCTGATGAGGTCTTACAGTCCTCTATGCCATGGTCACGACCATGCTGA  
 ACCCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG  
 GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

35 **AOLFR36 sequences:**

MYLVTVLNRNLLSILAVSSDSHPHTPMYFFLSNLWCADIGFTLATVPKMIVDMGSHSKVISYGG  
 CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS  
 WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFYDNTMFGFLPISGILLSYKIVPSILRIS  
 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAVAPPLRNGMVASVMYAVVTPMLNPFYIS  
 40 LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKQGPHSIPTSANPAP (SEQ ID NO: 67)

ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTCAGCTCTGACTCCC  
 ACCCCACACACCCATGTACTTCTTCTCTCAACCTGTGCTGGGCTGACATCGGTTTCACC  
 TTGGCCACGGTTCCCAAATGATTGTGGACATGGGGTGCATAGCAAAGTCATCTCTTATG  
 45 GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTCATGTATAGTAGACATGTTCTT  
 GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTGCCCCTTGCACTACCCAGTCATC  
 GTGAATCCTCACCTCTGTGTCTTCTTCGTTTGGTGCTCTTTTCTTAGCCTGTTGGATTCC  
 CAGCTGCACAGTTGGATTGTGTTACAATTACCTTCTTCAAGAATGTGGAAATCTCTAATT  
 TTGCTGTGAGCCATCTCAACTTCTCAAGCTTGCCTCTTATGACAGCGTCATCAATAGCATA  
 50 TATCAATATTTTGATAATACTATGTTTGGTTTTCTTCCCATTTTCAGGGATCCTTTTGTCTTAC  
 TATAAAATTGTCCCTCCATTCTAAGGATTTTCATCATCAGATGGGAAGTACAAAGCCTTCT  
 CAGCCTGTGGCTGTACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA  
 CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT  
 GTGGTCACCCCATGCTGAACCTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG  
 55 CCCTGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTCTTG

TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCCCTTAG  
(SEQ ID NO: 68)

**AOLFR37 sequences:**

5 MEKANETSPVMGFVLLRLSAHPELEKTFVLLILMYLVILLGNGVLILVTILDSRLHTPMYFFLG  
NLSFLDICFTTSSVPLVLDSTLPQETISFSACAVQMAISFAMAGTECLLSMMAFDYVAICNP  
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS  
INVISMEVTNVIFLGVPVLFISFSYVFIITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFFMYG  
KPKSKDSMGADKEDLSDKLIPLFYGVVTPMLNPIIYSLRNKDVKAAVRLLRPKGFTQ (SEQ ID  
10 NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC  
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT  
GGGCAATGGGGTCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCATGTAC  
15 TTCTTCCTAGGGAACCTCTCCTTCCTGGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT  
CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG  
GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGATC  
GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT  
GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTACACACATCCTTG  
20 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTCACTGTGAGATTCTGG  
CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA  
TGTGATCTTCTAGGAGTCCCGTTCTGTTTCATCTCTTCTCCTATGTCTTCATCATCACCA  
CCATCCTGAGGATCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA  
CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT  
25 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAACTCATCCCCCTTTCTATG  
GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG  
CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

**AOLFR38 sequences:**

30 MYLVTVLRLNLLILAVSSDSLHTPMCFFLSNLCWADIGFTSAMVPMIVDMQSHSRVISYAGC  
LTQMSFFVLFIACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVLVLVSFFLSLLDSQLHSW  
IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFIYLDSIMFGFLPISGILLSYANNVPSILRISS  
SDRKSKAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPPRNGVVASVMYAVVTPMLNPFYISLR  
NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

35 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC  
ACCTCCACACCCCCATGTGCTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC  
TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG  
CGGGCTGCCTGACACAGATGTCTTTCTTTGTCTTTTGCATGTATAGAAGACATGCTCCTG  
40 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTACCCCTGCACTACCCAGTCATCA  
TGAATCCTCACCTTGGTGCTTCTTAGTTTTGGTGCTCTTTTCTCAGCCTGTTGGATTCC  
CAGCTGCACAGTTGGATTGTGTTACAATTACCTTCTTCAAGAATGTGGAAATCTCCAATT  
TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCTGTTCTGACAGTGTCATCAATAGCATA  
TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTCAAGGATCCTTTTGTCTTAC  
45 GCTAACAAATGTCCCCTCCATTCTAAGAATTTTCATCATCAGATAGGAAGTCTAAAGCCTTCT  
CCACCTGTGGCTCTCACCTGGCAGTTGTTTGTCTTATTTATGGAACAGGCATTGGCGTGTA  
CCTGACTTCAGCTGTGTACACACCCCGAGGAATGGTGTGGTGGCATCAGTGATGTACGCT  
GTGGTCACCCCATGCTGAACCTTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG  
CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT  
50 CCATCCTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

**AOLFR39 sequences:**

MGVKNHSTVTEFLLSGLTEQAELQLPLFCLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS  
LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVCVISECYMLAAMACDRYVAICSP  
55 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIKHXYFCDIVPLIKLSCSSTYIDEL

LIFVIGGFNMVATSLTHISYAFILTSILRIHSKKGRCFAFSTCSSHLTAVLMFYGSLMSMYLKPAS  
SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)

5 ATGGGTGTAAAAAACCATTCCACAGTGACTGAGTTTCTTCTTTCAGGATTAAGTGAACAAG  
CAGAGCTTCAGCTGCCCCTCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG  
AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCCATGTACTAT  
TTCCTGAGTAGTTTGTCTTTTTAGATTTCTGCTATTCTTCTGTCAATTACCCCTAAAATGCT  
ATCAGGGTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTGAGCTGTTTT  
10 TTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC  
GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCCTAGGGTCTGTTCTCTGC  
TGGTGGCTGCTGCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT  
CAGGTTGTCTTTCTGTGGATCAAACATCATTAAACATTATTTCTGTGACATTGTCCTCTTA  
TTAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTGTCAATTGGTGGATTT  
AACATGGTGGCCACAAGCCTAACAATCATTATTTATATGCTTTTATCCTCACCAGCATCCT  
15 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCACCTGACA  
GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC  
ACTCACCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC  
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAACTTTAAGAAGA  
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

20

**AOLFR40 sequences:**

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS  
FIDMWFSTVTVPKMLMTLVSPSGRTISFHSQVAQLYFFHFLGSTECFLYTVMSYDRYLAI SYPL  
RYTNMMTGRSCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADTS  
25 ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVVLCFFGPGLFIYL  
RPGSRDALHGVAVFYTTLTPLFNPVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:  
75)

30 ATGTCCAACGCCACCCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC  
TGGACGCCCCCTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCA  
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTACGGTGCCCCAAAATGCTGATGAC  
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT  
TCCACTTCTTGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACCT  
35 GGCCATCAGTTACCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG  
GCCACCGGCACCTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC  
ATTTGCCCTACTGTGGACCCAACAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT  
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA  
GTGGCCTCGGGCTGCTTTGTCCTGATAGTGTCTGCTATGTGTCCATCGTCTGTTCATCCT  
40 GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC  
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGGACGC  
CTTGCATGGGGTTGTGGCCGTTTTCTACACCACGCTGACTCCTCTTTTCAACCCTGTTGTGT  
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAGTAT  
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

45

**AOLFR41 sequences:**

MNPENWTQVTSFVLLGFPSHLIQFLVFLGLMVYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN  
FSFLELLLVTVVVPKMLVVILTGDHTISFVSCIIQSYLYFFLGTTDFLLAVMSLDRLAICRPLR  
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFFRDSWPLRLRLSCGDTH  
50 LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAAERRKAFSTCASHLTVVVVIYGSIFLY  
IRMSEAQSKLLNKASVLSCIITPLNPFIFTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK  
(SEQ ID NO: 77)

55 ATGAACCCTGAAAACTGGACTCAGGTAACAAGCTTTGTCCTTCTGGGTTTCCCCAGTAGCC  
ACCTCATACAGTTCCTGGTGTTCCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG  
CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC

TTCCTGCGGAATTTCTCCTTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT  
 TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTCAGCTGCATCATCCAGTCCTACC  
 TCTACTTCTTTCTAGGCACCACTGACTTCTTCTCCTTGGCCGTCATGTCTCTGGATCGTTAC  
 CTGGCAATCTGCCGACCACTCCGCTATGAGACCTGATGAATGGCCATGTCTGTTCCCAAC  
 5 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCCTTTGCCCCACTGTCCTCATGGCC  
 AGCCTGCCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCTGTGACAGTTGGCCCTTGCT  
 CAGGCTTTCTTGTGGGGACACCCACCTGCTGAAACTGGTGGCTTTCATGCTCTCTACGTTG  
 GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTATGCCTGCATTCTTGCCACTGTTCT  
 CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTCCACTTGCGCCTCGCATCTTACA  
 10 GTGGTGGTCATCATCTATGGCAGTTCCATCTTTCTCTACATTCGTATGTCAGAGGCTCAGTC  
 CAAACTGCTCAACAAAGGTGCCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCCA  
 TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC  
 CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:

78)

#### 15 AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL  
 GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFFHFIGGIKIFLLTVMAYDRYIAISQPL  
 HYTLIMNQTVCALLMAASWVGGFHISVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDFTV  
 20 LELLMVSNNGLVTLMCFLVLLGSYALLVMLRSHSREGRSKALSTCASHIAVVTLFVPCIVVY  
 TRPFRTPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH  
 (SEQ ID NO: 79)

ATGAATCCAGCAAATCATTTCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT  
 25 GGGAGCTTCGGTTTGTCTTCTCTGCTGTGTATTTATGACTGTAGTGGGA  
 AACCTTCTTATTGTGGTCATAGTACCTCCGACCCACACCTGCACACAACCATGTATTTTCT  
 CTTGGGCAATCTTTCTTCTGACTTTTGCTACTCTTCCATCACAGCACCTAGGATGCTGG  
 TTGACTTGCTCTCAGGCAACCTACCATTTCTTTGGTGGATGCCTGACTCAACTCTTCTTC  
 TTCCACTTCAATTGGAGGCATCAAGATCTTCTGCTGACTGTCATGGCGTATGACCGCTACA  
 30 TTGCCATTTCCCAGCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT  
 ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC  
 AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT  
 CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTAACAATGGCCTG  
 GTGACCCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC  
 35 GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT  
 GGTGACCTTAATCTTTGTGCCTTGCATCTACGTCTATACAAGGCCCTTTTCGGACATTCCCCA  
 TGGACAAGGCCGTCTCTGTGCTATACAAATTGTCACCCCCATGCTGAATCCTGCCATCTA  
 TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG  
 ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

40

#### AOLFR43 sequences:

MQKPQLLVPIIATSNGNLVHAAYFLLVGIPGLGPTIHFVLAFLPLCFMYALATLGNLTIVLIIRVE  
 RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQIEFNICLAQMFLIHALSAVESAVLLA  
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWLSYCQHTHTVTHSFCLHQ  
 45 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRAALKAFNTCISHLCAV  
 LVFYVPLIGLSVVHRLGGPTSLLHVVMANTYLLLPVVNPLVYGAKTKEICSRVLCMFSQGGK  
 (SEQ ID NO: 81)

ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG  
 50 CAGCATACTTCCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACTTTTGGCTGGCT  
 TTCCCACTGTGTTTTATGTATGCCTTGCCACCCTGGGTAACTGACCATTTGCTCATCAT  
 TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGCGCATGCTTTCCACTATT  
 GACCTAGTCTCTCTCTATCACCATGCCCAAGATGGCCAGTCTTTTCTGATGGGCATCCA  
 GGAGATCGAGTTCAACATTTGCCTGGCCAGATGTTCTTATCCATGCTCTGTGAGCCGTG  
 55 GAGTCAGCTGTCCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCCATTTGCCACCCATTGC  
 GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG



GGGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCCTACTGCCAAACAC  
 ATACTGTCACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC  
 CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT  
 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCTCTCGGAGGGCA  
 5 GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC  
 CCTCATGGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCCATGTGGTT  
 ATGGCTAATACCTACTTGCTGCTACCACCTGTAGTCAACCCCTTGTCTATGGAGCCAAGA  
 CCAAAGAGATCTGTTCAAGGGTCCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID  
 NO: 82)

10

**AOLFR44 sequences:**

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERSLHAPMYLFLC  
 MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAJESTILLAMAFDRYVAICHPL  
 RHAAVLNNTVTAQIGIVAVVRGSLFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP  
 15 NVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAFYVPLIGLS  
 VVHRFGNSLHPIVRVVMGDIYLLPPVINPIIYGAKTKQIRTRVLAMFKJISCDKDLQAVGGK  
 (SEQ ID NO: 83)

ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA  
 20 AAGCCCATTTCTGGGTGGCTTCCCCCTCCTTTCCATGTATGTAGTGGAATGTTTGAAAC  
 TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTC  
 TCTGCATGCTTGACGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC  
 CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT  
 TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG  
 25 CCATCTGCCACCCACTGCGCCATGCTGCAAGTGTCAACAATACAGTAACAGCCCAGATTGG  
 CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC  
 TGGCCTTCTGCCACTCCAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA  
 GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC  
 ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTATTTTCTGATAATACGAACGGTTCTGC  
 30 AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTACACATTGGTGT  
 GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAACAGC  
 CTTTCATCCCATTTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAA  
 TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG  
 ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

35

**AOLFR45 sequences:**

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIIQADAALHEPMYLFLA  
 MLATIDLVLSSSTLPKMLAIFWFRDQEINFFACLQMFLLHSFSIMESAVLLAMAFDRYVAICKP  
 LHYYTTLTGLITKIGMAAVARAATLMTPLPFLRRFHYCRGPVIAHCYCEHMAVVRACGDT  
 40 SFNNIYGIAMFVSVLDLLFVILSYVFLQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS  
 SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIIYGKTKQIREYVLSLFQRKNM (SEQ ID NO:  
 85)

TGGAAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTGAACTCTAATCATATATA  
 45 CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTC  
 GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT  
 TCCTGGTTTGGAAACACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG  
 CCTGCTAGGCAACTGTACCTTCTCTTATTATCCAGGCTGATGCAGCCCTCCATGAACCC  
 ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTTCTTTCTTACAACGCTGCC  
 50 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTGCCTGTCTGGTC  
 CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTT  
 TGACCGCTATGTGGCCATCTGCAAGGCTATGCATACACGACGGTCTGACTGGGTCCCTC  
 ATCACCAGATTGGCATGGCTGCTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCT  
 TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGCTACTGTGAACA  
 55 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT  
 GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT



TCAGGCAGTTCTCCAGCTTGCCTCTCAGGAGGCCCCGCTACAAAGCATTGGGACATGTGTG  
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCCCG  
TGAGCCCCGCCATGCTGCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCTTTTCC  
CAGCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTCTGTGAGTATGTGCT  
5 CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA  
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAAATTGCAGAGT  
ATCTTTGACAATTCTCTAGTATGATAAGGAAAAATGAGGTTTCATTCCTCACAGATCTACGA  
GTCAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA  
TTGTCATAGACTCATCACATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG  
10 GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID  
NO: 86)

#### AOLFR46 sequences:

MNIKHCGWHMIHTWLNIREDDSDFKNFQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV  
15 SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLLAMGANTLLITIQLAS  
LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFDLRSISFPACFLQMFIMNSFLTMESCTFMVMA  
YDRYVAICHPLRYPSTIDQFVARAVFVIARNAFVSLPVPML SARLRYCAGNIKNKICSNLSVS  
KLSCDDITFNQLYQFVAGWTLGSDLILIVISYSFILKVVLRIKAEGAVAKALSTCGSHFILILFFS  
TVLLVLVITNLARKRIPDPVILLNLHLLPALNPVYGVRTKEIKQIQNLKRL (SEQ ID NO:  
20 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT  
GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAACCCACACT  
CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTAAAGGTACAC  
25 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC  
CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT  
CTGCCCTCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT  
CCAGCTGGAGGCCTCTCTGCACCAGCCCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGG  
ACATCGTGTCTCTGCCTCACCGTCATCCCCAAGTCTGGCCATCTTCTGGTTTGACCTCAGG  
30 TCGATCAGCTTCCCAGCCTGCTTCTCCTCCAGATGTTTCATCATGAACAGTTTTTGGACCATGGA  
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA  
TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA  
ATGCCTTTGTTTCTCTTCTGTTCCCATGCTTTCTGCCAGGCTCAGATACTGTGCAGGAAAC  
ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAACTCTCTTGTGATGACATCA  
35 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT  
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT  
GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTCAGCACAGTCC  
TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCCTCCAGATGTCCCCATCCT  
40 GCTCAACATCCTGCACCACCTCATTCCCCAGCTCTGAACCCCATTTGTTTATGGTGTGAGA  
ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

#### AOLFR47 sequences:

MSASNTLTHPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIQADAALHEPMYLFLA  
MLAAIDLVLSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK  
45 PLHYTKVLTGSLITKIGMAAVARAVTLMPLPFLRLCFHYCRGPVIAHCYCEHMAVVRLACGD  
TSFNNIYGIAVAMFIVLDLLLVILSYIFILQAVLLLASQEARYKAFGTCVSHIGAILAFYTTTVIS  
SVMHRVARHAAPHVHILLANFYLLFPPMVNPIHYGVKTKQIRESILGVFPRKDM (SEQ ID NO:  
89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTTGTGGTGGGGATTCCAG  
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG  
CTTGAAACTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT  
ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTCTCCTCCTCAGCACTGCCAAA  
ATGCTTGCCATATTCTGGTTCAAGGATCGGGAGATAAACTTCTTTGCTGTCTGGCCAGGA  
55 TGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGTGCTGGCCATGGCCTTTGAC  
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA

CCAAGATTGGCATGGCTGCTGTGGCCCCGGGCTGTGACACTAATGACTCCACTCCCCTTCTCT  
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG  
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG  
CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATTCTTCAG  
5 GCAGTTCTACTGCTTGCTCTCAGGAGGCCCGCTACAAGGCATTGGGGACATGTGTCTCTC  
ATATAGGTGCCATCTTAGCCTTCTACACAAGTGTGGTCATCTCTCAGTCATGCACCGTGTA  
GCCCGCCATGCTGCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC  
CATGGTCAATCCATAATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGA  
GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

10

**AOLFR48 sequences:**

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTHYIVRTEHSLHEPMYIFL  
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFHLSLSGMESTVLLAMAFDRYVAICH  
PLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI  
15 RVNVVYGLIIVISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFGLSM  
VHRFSKRDRSPLPVILANYLLVPPVLNPVYGVKTKAIRQLRLRFHVATHASEP (SEQ ID NO:  
91)

ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC  
20 CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT  
GTGCTAGGTAACCTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA  
TGTATATATTTCTTTCATGCTTTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCC  
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA  
GATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCGCCATGGCTTTT  
25 GACCGCTATGTGGCCATCTGTACCCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG  
TCACCAAAATTGGTGTGGCTGCTGTGGTGGGGGGGCTGCACTGATGGCACCCTTCTCTGT  
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTCCCATTCTACTGCCTACACC  
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT  
CATCATCTCCGCCATTGGCCTGGACTCCTTCTCATCTCCTTCTCATATCTGCTTATTCTTA  
30 AGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCCAAGGCATTTGGCACTTGCGTCTCTCA  
TGTGTGTGCTGTGTTTATATCTATGTACCTTTTATTGGATTGTCCATGGTGCATCGCTTTA  
GCAAGCGGCGTGACTCTCCGCTGCCGCTCATCTTGGCCAATATCTATCTGCTGGTTCCTCCT  
GTGCTCAACCAATTGTCTATGGAGTGAAGACAAAGGAGATTGACAGCGCATCCTTCGA  
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

35

**AOLFR49 sequences:**

MLTFHNVCSPSSFWLTGIPGLES�HVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF  
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDAQLGQMFLIHCATVESGIFLAMAFDRYVAIC  
NPLRHSMLVLTYYTVVGRGLVSLRLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALT  
40 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKTGTGASHLCAILIFYVP  
IAVSSLIHRFGQCVPPVHTLLANFYLLIPPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID  
NO: 93)

ATGCTCACTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG  
45 GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG  
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG  
TACTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTCTGTCTACTTCCACTATAACCCAA  
ACTTCTGGGAATCTTCTGGTTCGGTGCTTGTGACATTGGCCTGGACGCCTGCTTGGGCCAA  
ATGTTCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCTTGGCATGGCTTTTGA  
50 TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG  
GGTCGTTTGGGGCTTGTCTCTCCTCCGGGTGTTCTCTACATTGGACCTCTGCCTCTGAT  
GATCCGCCTGCGGCTGCCCTTTATAAAACCCATGTTATCTCCCACTCCTACTGTGAGCAC  
ATGGCTGTAGTTGCCCTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC  
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT  
55 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC  
TTCTCACCTCTGTGCCATCCTGATCTTTTATGTTCCCATGCTGTTTCTTCCCTGATTCACCG

ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTC  
CTCCAATCCTCAATCCCATTGTCTATGCTGTTTCGCACCAAGCAGATCCGAGAGAGCCTTCT  
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

5 **AOLFR50 sequences:**

MNLDSFFSFLKSLIMALSNSSWRLPQPSFVLVGIPLGLESQHWIALPLGILYLLALVGNVTILFI  
WMDPSLHQSMYLFSLMLAIDL VVASSTAPKALAVLLVRAQEIGYTVCLIQMFFTHAFSSMES  
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLIPFLILLRKLIFCQATIIGHAY  
CEHMAVVKLACSETTVNRAYGLTVALLVVGDLVLAIGVSYAHILQAVLKVPGNEARLKAFST  
10 CGSHVCVILVFYIPGMFSFLTHRFGHHVPHVHVLLAILYRLVPPALNPLVYRVKTQKIHQ  
(SEQ ID NO: 95)

ATGAATTTGGATTCTTTTTTCTCTTTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC  
CAGCTGGAGGCTACCCAGCCTTCTTTTTTCTGGTAGGAATCCGGGTTTAGAGGAAAGC  
15 CAGCACTGGATCGCACTGCCCTGGGCATCCTTTACCTCCTTGCTCTAGTGGGCAATGTTA  
CCATTCTCTTCATCATCTGGATGGACCCATCCTTGACCAATCTATGTACCTCTTCTGTCC  
ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCACTGC  
TCCTGGTTTCGTGCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTCACCCAT  
GCAATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA  
20 TTTGTCACCCCTTGCACTTCCACAATCCTGCATCCAGGGGTATAGGGGCACATCGGAAT  
GGTGGTGTGGTGGGGGATTACTACTCCTCATCCCCTTCTCATTCTGTTGCGAAAACCTT  
ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC  
TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT  
TGGGCTGGATGTCCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG  
25 GTACCAGGAAATGAGGCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTTGTGTCA  
TCCTGGTCTTCTATATCCCGGAATGTTCTCCTTCTCACTACCGCTTTGGTTCATCATGTA  
CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGCGCCACCTGCACTCAATCC  
TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

30 **AOLFR51 sequences:**

MCQQILRDCILLIHLICNRKKVSLVMLGPAYNHTMETPASFLLVGIPLQSSHLWLAISSLAM  
YIALLGNTIIVTAIWMDSTRHEPMYCFCLVLAVIDIVMASSVVPKMSVIFCSGDSISFSACFTQ  
MFFVHLATAVETGLLLTMAFDYVAICKPLHYKRILTPQVMLGMSMAITRAIIATPLSWMVS  
HLPFCGSNVVHSYCEHIALARLACADVPSSLYSLIGSSLMVGSVDVAFIAASYILILKAVFGLSS  
35 KTAQLKALSTCGSHVGMALYYLPGMASIYAAWLQDQDVVPLHTQVLLADLYVIIPATLNPPIY  
GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA  
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC  
40 CTTCCTCCTTGTGGGTATCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA  
GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA  
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA  
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG  
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG  
45 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA  
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT  
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT  
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA  
GCAGTCTCTACAGTCTGATTGGTTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT  
50 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA  
AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG  
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCAAAGTCCTGC  
TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC  
CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCTCTTTGACCATTCCAAC  
55 CTGGGTTTCATGA (SEQ ID NO: 98)

**AOLFR52 sequences:**

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYITALLGNTLIVTAIWMDSTRHEPMY  
 CFLCVLAAVDIVMASSVVPKMVSIFCSGSSISFSACFTQMFFVHLATAVETGLLLTMAFDTRYV  
 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLPCGSNVVHSHYCKHIALAR  
 5 LACADVPVSSLYSLIGSSLMVGSDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGVMA  
 YLPGMASIYAAWLQDIVPLHTQVLLADLYVIIPATLNPITYGMRTKQLLEGIWSYLMHFLFDH  
 SNLGS (SEQ ID NO: 99)

ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCTCCTTGTGGGTA  
 10 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC  
 AGCCCTGTTAGGAAACACCCTCATCGTGACTGCAATCTGGATGGATTCCACTCGGCATGAG  
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT  
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC  
 ACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG  
 15 CTTTGGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCAGCCTCA  
 AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTGACTCCACTG  
 AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTGTCCACTCCTACTGTAA  
 GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG  
 ATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT  
 20 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT  
 GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG  
 CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCCAAGTGCTGCTAGCTGACCTGTACGT  
 GATCATCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG  
 GGAATATGGAGTTATCTGATGCACCTCCTTTGACCACTCCAACCTGGGTTTCATGA (SEQ  
 25 ID NO: 100)

**AOLFR54 sequences:**

MSDSNLSDNHLPDTFFLTGIPGLEAAHFVIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY  
 LFLCLLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA  
 30 ICNPLRYTTILNHA VIGRIGFVGLFRSVAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGRIARLACA  
 NITVNIVYGLTVALLAMGLDSILIAISYGFIHVAVFHLPSHDAQHKALSTCGSHIGILVFYIPAFF  
 SFLTHRFHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID  
 NO: 101)

ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC  
 35 CAGGGCTGGAGGCTGCCCACCTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC  
 ACTGGTTGGAAATGCTGCCCTCATCCTGGTCATTGCCATGGACAATGCTCTTCATGCACCT  
 ATGTACCTCTTCTCTGCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC  
 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCCTGGCC  
 40 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCCTCGATTCTACTTGCCATGGCCTT  
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTTCTCAACCATGCTGTC  
 ATAGGCAGAATTGGCTTTGTGGGCTTATCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT  
 CTTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTGATGACACACACATACTGTGAGCAT  
 ATGGGCATCGCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG  
 45 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC  
 CATGCAGTCTTTACCTTCCATCTCATGATGCCCAGCACAAAGCTCTGAGTACCTGTGGCT  
 CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCCCTACCCACCGC  
 TTTGGTCACCACGAAGTCCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG  
 TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTGGGAGTCGACT  
 50 TCTAAACTGCTTACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

**AOLFR57 sequences:**

MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQNKNIENVLCFVLFVLCYIAIWMGNLLIMISITCTQ  
 LIHQPMYFFLNYSLSLDCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEIFILTGM  
 55 AYDRYVAICKPLHYTIIMSROKCNTHIVCCTGGFIHSASQFLLTIFVPFCGPNEIDHYFCDVYPLL  
 KLACSNHMIIGLLVIANSGLIALVTFVLLLSYVFILYTIIRAYSAERRSKALATCSSHVIVVVLFF

APALFIYIRPVTTFSEDKVFALFYTHAPMFNPLIYTLRNTEMKNAMRKVWCCQILLKRNLQF  
(SEQ ID NO: 103)

5 ATGTCATTTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAGCAATAATA  
GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAATAAGAACATTGAAGTCCTCTGCTTTGTA  
TTATTTTTGTTTTGCTACATTGCTATTTGGATGGGAACTTACTCATAATGATTCTATCAC  
GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCTCAATTACCTCTCACTCTCCGACC  
TTTGCTACACATCCACAGTGACCCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC  
10 CATTTCTATAATAAAGTGTATGATACAACCTCTTACCACCCATTTTTTTGGAGGCATAGAGA  
TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTGCAAGCCCTGCACTA  
CACCATTATTATGAGCAGGCAAAAGTGTAAACACAATCATCATAGTTTGTGTTGACTGGGGGA  
TTTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTTGTGGCCCAAATGA  
GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA  
TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG  
15 TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA  
AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTTGCTCCTGCATTG  
TTCATTTACATTAGACCGGTCACAACATTCTCAGAAGATAAAGTGTGTCCTTTTTTATAC  
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC  
GCCATGAGGAAAGTGTGGTGTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ  
20 ID NO: 104)

**AOLFR58 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF  
VLLGLSQPNPVQEIVFVFLFVYIATVGGNMLIVVILSSPALLVSPMYFFLGFLSFLDACFSSVI  
25 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL  
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS  
FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA  
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

30 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTGCACTTGGATGTACCAACTTGTTAA  
TGACTATGATACCACAAATTGATCTGAAGCAAAATTTCCCTTTGTCCTAATTGCAGACTATA  
CATGATCCCTGTTGGAGCTTTCATCTTTTCCCTTGGGAAACATGCAAAACCAAAGCTTTGTA  
ACTGAGTTTGTCTCCTGGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG  
TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTCTC  
35 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCCTTCTGGA  
TGCGTGCTTCTCATCTGTCATACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA  
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG  
AGGTGATTGTCCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA  
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG  
40 GGCTCTTGCAATCCATGATACAAATCTTTTACTTTTCCAGCTTCCCTTTTGTGGCCCCAA  
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCTGCACTGATACTC  
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG  
TTGCTTGTCTCCTATGCTGTCATCTTGCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG  
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA  
45 TATTTGTATATACAGACCTCCATCTGCTTTTTCCCTTGACAAAATGGCGGCAATATTTTAT  
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTTCAGGAATAAGGAAGTAAAC  
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA  
AACTTTAA (SEQ ID NO: 106)

**AOLFR59 sequences:**

MGDWNNSDAVEPIFILRGFPGLEYVHSWLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYYFI  
SILAVNDLGMSLSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH  
PLHYPTILNSVIGKIGLACLLRSLGVVLPPLLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA  
RTNSIYGLCVVIATLGVDSIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLFFVPVIGVS  
55 MVHRFGKHLSPIVHILMADIYLLPVLNPIVYSVRTKQIRLGILHKFVLRRRF (SEQ ID NO:  
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCTTG  
 GACTGGAGTATGTTCAATCTTGGCTCTCCATCCTCTTCTGTCTTGCATATTTGGTAGCATTT  
 ATGGGTAATGTTACCATCCTGTCTGTCAATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA  
 5 TACTTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCCACCA  
 TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT  
 GTTCTTCATCCACACATTCACATTCCTGGAGTCCCTCAGTGTTGCTGGCCATGGCCTTTGACC  
 GTTTTGTTGCTATCTGCCATCCACTGCACTACCCACCATCCTCACCAACAGTGTAATTGGC  
 AAAATTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTAATTTCCACACCTTTGCTACT  
 10 GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGCACCAGGAT  
 GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA  
 TTGCCACACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT  
 GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCATA  
 TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG  
 15 AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTTCCCCCAGT  
 CCTTAACCTATTGTCTATAGTGTGAGAACAAGCAGATTCTGTCTAGGAATTCTCCACAAG  
 TTTGTCCTAAGGAGGAGGTTTAA (SEQ ID NO: 108)

**AOLFR60 sequences:**

20 MFLPNDTQFHPSSFLLLGLIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMFYFLA  
 MLATTDVGLSTATIPKMLGIFWINLRGHIIEACLTQMFFIHNFTLMESA VLVAMA YDSYVAICN  
 PLQYSAILTNKVSVSIGLVFVRALIFVIPSILLILRPF CGNHVIPHTYCEHMG LAHLSCASIKINI  
 IYGLCAICNLVFDITVIALSYVHILCAVFRLP THEPRLKSLSTCGSHVCVILAFYTPALPFSFMTHC  
 25 FGRNVPRYIHILLANLYVVPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF  
 (SEQ ID NO: 109)

ATGTTCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG  
 ACTAGAAACACTTCACATCTGGATCGGCTTTCCTTCTGTGCTGTGTACATGATCGCACTC  
 ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT  
 30 TCTACTTCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA  
 GATGCTTGGAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG  
 ATGTTTTTTATCCACAACCTTCACACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG  
 ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCAACAAGGTTGT  
 TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCAATCCCTCTATACTTC  
 35 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCCCCACACCTACTGTGACACAT  
 GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTATTTATGTGCCA  
 TTTGTAATCTGGTGTGTTGACATCACAGTCAATGCCCTCTCTTATGTGCATATTCTTTGTGCT  
 GTTTCGGTCTTCTTCTACTCATGAGCCCGACTCAAGTCCCTCAGCACATGTGGTTCACATGT  
 GTGTGTAATCCTTGCCCTTCTATACACCAGCCCTCTTTTCTTATGACTCATTGCTTTGGCC  
 40 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT  
 GCTCAATCCTGTCTATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT  
 ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA  
 (SEQ ID NO: 110)

**AOLFR61 sequences:**

45 MSIINTSYVEITTFFLVGMPGLEIAHIWISIPICSMYLIAILGNGTILFIKTEPSLHGPMYYFLSML  
 AMSDLGLSLSSLPTVLSIFLNA PETSSSACFAQE FFIHGFSVLESSVLLIMSFDRFLAIHNPLRYT  
 SILTTVRVAQIGIVFSFKSM LVL PFPFTLRSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY  
 GFFGALCLMVDFILIAVS YTLILKTVPGIASKKEELKALNTCVSHICAVIIFYLPINLAVVHRFAG  
 50 HVSP LINVLMANVLLVPPLMKPIVYCVKTKQIRVRVVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG  
 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT  
 CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCCATGT  
 55 ACTATTTTCTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT  
 GTGTAAAGCATCTTCTGTTCAATGCCCTGAAACTTCTTCTAGTGCTGCTTTGCCAGGA



ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA  
 GATTCCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACCTGTCAGAGTTGC  
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT  
 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA  
 5 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA  
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT  
 ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC  
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG  
 GCATGTCTCTCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA  
 10 TGAAACCAATTGTTTATTGTGTAATAAAGAGATTAGAGTGAGAGTTGTAGCAAAATT  
 GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

#### AOLFR62 sequences:

MFYHNKSIFHPVTFFLIGIPGLED FHMWISGPFCSVYLVALLG NATILLVIKVEQTLREPMFYFL  
 15 AILSTIDLALSATSVPRMLGIFWFD AHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC  
 APLHYATILTSVLV GISM CIVRPVLLT LPMVYLIYRLPFCQAHIHAHSYCEHMGIAKLSCGNIRI  
 NGIYGLFVVSFFVLNLVLIGISYVYILRAVFR LPSHDAQLKALSTCGAHVGVICVFYIPSVFSLT  
 HRFQHQIPGYIHILVANLYLIIPPSLNPIIYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

20 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTTCCTCATTGGAATCCCAGG  
 TCTGGAAGACTTCCACATGTGGATCTCCGGGCCTTTCTGCTCTGTTTACCTTGTGGCTTTGC  
 TGGGCAATGCCACCATCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT  
 CTA CTCTCCTGGCCATTCTTTCCACTATTGATTTGGCCCTTTCTGCAACCTCTGTGCCTCGCA  
 TGCTGGGTATCTTCTGGTTTGATGCTCAGGATTA ACTATGGAGCTTGTGTGGCCAGAT  
 25 GTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC  
 CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGGT  
 GGGCATTAGCATGTGCATTGTAATTCGTCCTGTTTACTTACACTTCCCATGGTCTATCTTA  
 TCTACCGCCTACCTTTTGTGAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG  
 CATTGCAAAATTGTCTGTGGAAACATTGCTATCAATGGTATCTATGGGCTTTTTGTAGTTT  
 30 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC  
 TTCCGCCTCCCATCATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG  
 GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTCTTCTTACTCATCGATTTGGACAC  
 CAAATACCAAGTTACATTACATTCTTGTGTTGCCAATCTCTATTTGATTATCCCACCTCTCT  
 CAACCCCATCATTTATGGGGTGAGGACCAACAGATTCGAGAGCGAGTGCTCTATGTTTTT  
 35 ACTAAAAAATAA (SEQ ID NO: 114)

#### AOLFR63 sequences:

MSINTSYVEITTFVLVGM PGL EYAH I WISIPICSMYLIAILNGN TILFIKTEPSLHEP MY YFLSML  
 AMSDLGLSLSSLPTVLSIFLNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYTS  
 40 ILTTVRVAQIGIVFSFKSMLLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY  
 GFFGALCLMVDFILIAVSYTLILKTVLGLASKKEQLKALNTCVSHICAVIIFYLPINLAVVHRFAR  
 HVSPLINVL MANVLLL VPPLTNPIVYCVKTKQIRVRV VAKLCQRKI (SEQ ID NO: 115)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG  
 45 GGCTAGAATATGCACACATCTGGATCTCTATCCCATCTGCAGCATGTATCTTATTGCTATT  
 CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT  
 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT  
 GTGTTAAGCATCTTCTGTTCAATGCTCCTGAAATTTTCATCCAATGCCTGCTTTGCCAGGA  
 ATTCTTCATTGATGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA  
 50 GATTCCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACCTGTCAGAGTTGC  
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT  
 TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA  
 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA  
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT  
 55 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC  
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG

GCATGTCTCTCCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA  
CGAACCCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT  
GTGTCAACGGAAGATTTAA (SEQ ID NO: 116)

5 **AOLFR64 sequences:**

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTIVILGNLTILHVICTDATLHGPMYYFLG  
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL  
HDSTVLTPACIVKMGLSSVLRALLILPLPFLLRKFQYCHSHVLAHAYCLHLEIMKLACSSIIVN  
HIYGLFVVACTVGVDLLIFLSYALILRTVLSIAHQERLRALNTCVSHICAVLLFYIPMIGLSLV  
10 HRFGEHLPRVVHLFMSYVYLLVPPLMNPFIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID  
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAG  
GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC  
15 TTGGGGAACCTCACCATTCTCCACGTCAATTTGTACTGATGCCACTCTCCATGGACCCATGT  
ACTATTTCTTGGGCATGCTAGCTGTCACAGACTTAGGCCTTTGCCTTTCCACACTGCCCACT  
GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC  
TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC  
CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCCTGACACCTGCATGTATTG  
20 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCTTGCCATTCTCTC  
CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACTGGA  
GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG  
GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCCTTCGCAC  
CGTGCTCAGCATTGCCTCCCACAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT  
25 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG  
TGAACATCTGCCCCGCGTTGTACACCTTCTCATGTCTATGTGTATCTGCTGGTACCACCCC  
TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAGAA  
GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

30 **AOLFR65 sequences:**

MAGRMSTSNHTQFHPSSFLLLGIPGLEDVHIWIGVPFFFVYLVALLGNTALLFVIQTEQSLHEPM  
YYFLAMLDSIDLGLSTATIPKMLGIFWFNTKEISFGGCLSHMFFIHFHTAMESIVLVAMAFDRYI  
AICKPLRYTMILTSKHSIAGIAVLRSLYMVVPLVFLRLPFCGHRIIPHTYCEHMGIA RLACAS  
IKVNIRFGLGNISLLLLDVILILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL  
35 THRFHNPQYIHIILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCCCTACTGCT  
GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTTCTTTGTGTAT  
CTTGTGCACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC  
40 ATGAGCCTATGTACTACTTCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC  
CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTTGGAGGC  
TGCTTTTCTCATATGTTCTTCATCAATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC  
CATGGCCTTTGACCGCTACATTGCCATTGCAAACCTCTTCGGTACACCATGATCCTCACCA  
GCAAATCATCAGCCTCATTGCAGGCATTGCTGTCCTGAGGAGCCTGTACATGGTTGTTCC  
45 ACTGGTGTCTCTCTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT  
GTGAGCATATGGGCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG  
CCTTGGAACATATCTCTCTTGTACTGGATGTTATCCTTATTATTCTCTCCTATGTGAGGA  
TCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT  
GGTTCTCATATTGGTGTATCTTAGCCTTTTTTACACCAGCATTITTTTCATTCTTGACACA  
50 TCGTTTTGGCCATAATATCCACAGTATATACATATTATATTAGCCAACCTGTATGTGGTTG  
TCCCACCAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTTCGAGAGAGAG  
TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

**AOLFR66 sequences:**

55 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL  
ALLSFTDVLMTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMLMALDHCVAI



CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN  
VRVNAIYGLIVALLIGGFDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF  
TFFTHHFGGHTIPLHHIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ  
ID NO: 121)

5

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTCATCCTAAATGGCATCCCTG  
GTTTGGAAGATGTGCATTTGTGGATCTCCTCCCACCTGTGTACCATGTACAGCATTGCTATT  
ACAGGGAACCTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT  
ATGCTTCCCTTGCCCTTCTTTCCCTTACAGATGTGCTCATGTGCACCAGCACCCTTCCCAAC  
10 ACTCTCTTCATAITGTGGTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCCAGAT  
GTTCTTTGTGCACACCTTACAGGGATGCGTGTGGGGTGCTCATGCTCATGGCCCTGGAC  
CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC  
TAAAGCTGGGTTCCCTCACTTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTTCTCTCA  
CCAAGCGCCTTCCATACTGCAAGGGCAACGTCATACCCACACCTACTGTGACCACATGTC  
15 TGTGGCCAAGATATCTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC  
CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC  
AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCAC  
TTCTGTGCCATAGTCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG  
GGGACACACCATTCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC  
20 CCACAATGAACCCTATTGTGTATGGGGTGAACCAGGCAGGTACGAGAAAGTGTCAATTA  
GGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

#### AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYILA VVGNCGLICLISHEEALHRPMYYFLA  
25 LLSFTDVTLCCTMVPNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVLMLMALDRYVAI  
CYPLRYATILTNPVIAKAGLATFLRNVMLIIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN  
FKVNAIYGLMVALLIGVFDICISVSYTMILQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAF  
FTFFTHRFVGHNPNIHIIIVANLYLLLPTMNPVYGVKTKQIQEGVIKFLLDGKVSFTYDK  
(SEQ ID NO: 123)

30

ATGTCTGGGGACAACAGCTCCAGCCTGACCCAGGATTCTTTATCTTGAATGGCGTTCCTG  
GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC  
GTGGGGAACCTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT  
ACTACTTCCCTGGCCCTGCTCTCCTTCACTGATGTCACCTTGTGCACCACCATGGTACCTAAT  
35 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCGAGA  
TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA  
CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG  
CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCATTCACTCTCCTC  
ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTTCATCCCCACACCTACTGTGACCATATGT  
40 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC  
TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG  
CTGTTATGAGCCTGTGCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA  
CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTTGT  
AGGACACAATATCCCAAACCACATACATCATCGTGGCCAACCTTTATCTGCTACTGCCT  
45 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTTCAGGAAGGTGTAATTA  
AATTTTTACTTGAGACAAGGTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

#### AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLFLAVGANTTLLMTIWLEASLHQPL  
50 YYLLSLLSLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCF LAMESCTFMVMAYDRY  
VAICHPLRYPSTIDHFVVKAAMFILTRNVLMTLPIPILSAQLRYCGRNVIENCICANMSVSRISC  
DDVTINHL YQFAGGWTLGSDLILIFLSYFILRAVRLKAEGAVAKALSTCGSHFMLILFFSTIL  
LVFVLTHVAKKVVSPDVPVLLNVLHHVIPAALNPIYGVRTQEI KQGMQRLLKKGC (SEQ ID  
NO: 125)

55

ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT  
 TTGTCAGATCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCCTCAGCCTCCTTTTCTCTTG  
 GCCGTAGGGGCCAACACCACCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC  
 CCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC  
 5 CCGAAGGTCCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCCCT  
 CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGACATTCATGGTCATGGCC  
 TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT  
 TGTAAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCCATCCCC  
 ATCCTTTTCAACACAACCTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA  
 10 ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT  
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCTACACCTTCATTCT  
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG  
 CTCCCACTTCATGCTCATCCTCTTCTCAGCACCATCCTTCTGGTTTTTGTCTCACACATGT  
 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT  
 15 CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCCAAGAAATTAAGCAGGGAATG  
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

#### AOLFR69 sequences:

MSYSIYKSTVNIPLSHGTVVHSFCHNMNCFMHIFKVLDFNMKNVTEVTLFVLKGFTDNLELQ  
 20 TIFFFLFLAIYLFITLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTKN  
 KVISFLGCVAQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYVPLINASYVAGI  
 LHATHTVATFSLFCGANEIRRVFCDPPLLAISYSDTHTNQLLLFYFVGSIELVTILIVLISYGLIL  
 LAILKMYSAEGRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHDMIVSIFYTIVIPLLNPV  
 IYSLRNKDVKDSMKMFMFGKNQVINKVYFHTKK (SEQ ID NO: 127)  
 25  
 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTGTTTCATT  
 CTTTTTGTGATAATATGAAGTGAAGTTTATGCATATCTTCAAGTTTGTCTAGATTTCAAC  
 ATGAAGAATGTCACTGAAGTTACCTTATTTGTAAGGCTTACAGACAATCTTGAAC  
 TGCAGACTATCTTCTTCTCCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA  
 30 GGACTGATTTTAGTGGTCAATTAGGGATTCCCAGCTCCACAAACCATGTACTATTTCTGA  
 GTATGTTGTCTTCTGTGGATGCCTGCTATTCTCAGTTATTACCCCAAATATGTTAGTAGAT  
 TTTACGACAAAGAATAAAGTCATTTTCTTGGATGTGTAGCACAGGTGTTTCTTGCTT  
 GTAGTTTTGGAACACAGAATGCTTTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC  
 CATCTACAACCTCTCCTGTATTAGTGAGCATGTACCCAGAGTCTACATGCCACTCATC  
 35 AATGCTTCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT  
 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTTGTGATATCCCTCCTCTCCTTGCTA  
 TTTCTTATTCTGACACTCACACAAACAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG  
 CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTTGATTCTGTTGGCCATTCTGAAGAT  
 GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTACCTAAGTGGAGT  
 40 GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTTCAGCTATGCTCG  
 GACCATGACATGATAGTGTCAATATTTACACCATGTGATTCCCTTGCTGAATCCCGTCAT  
 CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA  
 GGTATCAATAAAGTATATTTTCACTACTAAAAAATAA (SEQ ID NO: 128)

#### AOLFR70 sequences:

MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI  
 YLFTLIGNLGLVVLVIEDSWLHNPMMYYFLSVLSFLDACYSTVVPKMLVNFLAKNKSISFIGCA  
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASVYVAGILHATHIVA  
 50 TFSLSFCGSNEIRHVFCMPPLLAISCSDTHTNQLLLFYFVGSIEIVTILIVLISCDIFILLSILKMHS  
 KGRQKAFSTCGSHLTGVTIYHGTLVSVMRPSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK  
 KAVKKMLKLVYK (SEQ ID NO: 129)

ATGGACTCCACTTTACAGGCTATAACCTTTATAACCTGCAAGTAAAACTGAAATGGACA  
 AGTTGTCATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA  
 55 TGTTTATATTGACAGGCTTACAGATGATTTTGTAGCTGCAAGTCTTCTATTTTACTATTT  
 TTTGCAATCTATCTCTTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG

5 ATTCCTGGCTCCACAACCCCATGTATTATTTTCTTAGTGTTTTATCATTCTTGGATGCTTGC  
 TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGGCAAAAAATAAATCCATTT  
 CATTTATCGGATGTGCAACACAGATGCTTCTTTTTGTTACTTTTGGAACTACAGAATGTTTT  
 CTCTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCCTCTCCTGTATTCACT  
 10 GAGCATGTCACCCAGAGTCTATGTGCCACTCATCACTGCTTCCTACGTTGCTGGCATTTTAC  
 ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCCTTCTGTGGATCCAATGAAATTAG  
 GCATGTCTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC  
 AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGTCCTCATT  
 TCCTGTGATTTCACTTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG  
 15 CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAATTTATCATGGAACAATTTCTCGTC  
 AGTTATATGAGACCAAGTTCCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT  
 ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA  
 AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

15 **AOLFR71 sequences:**

MGRNNTNVPDFILTGLSDSEEVQMALFILFLIYLITMLGNVGMILIRLDLQLHTPMYFFLTH  
 LSFIDLSYSTVITPKTLANLLTSNYISFMGCFMQMFFVFLGAAECFLSSMAYDRYVAICSPRLY  
 PVIMSKRLCCALVTGPYVISFINSFVNVVWMSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI  
 20 MIHILAGSTLMVSLITISASYVLSILSTILKINSTSGKQKALSTCASHLLGVTIFYGTMIFTYLPKPK  
 SYSLGRDQVASVFYTVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

25 ATGGGTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG  
 AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC  
 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATTGATTTTT  
 TCCTTACTCACTTGTCAATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA  
 GCGAACTTACTGACTTCCAATATATTTCTTCTCATCAATGGCCTATGATCGCTACGTAG  
 TGTCTTCTGGGAGCTGCTGAATGTTTTCTTCTCATCAATGGCCTATGATCGCTACGTAG  
 CTATCTGCACTCCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC  
 30 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC  
 TGCATTTCTGCGACTCAAATGTAGTTCGTCACITTTTCTGCGACACGCTCTCCAATTTTAGCT  
 CTGTCTGCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC  
 TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCCTGAAA  
 ATTAATTCACCTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG  
 TCACCATCTTTTATGGAACATGATTTTTTACTTATTTAAAACCAAGAAAGTCTTATTCTTGT  
 35 GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT  
 TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA  
 GGACTCCAGGTAA (SEQ ID NO: 132)

**AOLFR72 sequences:**

40 MAPENFTRVTEFILTVSSCPQLPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL  
 ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL  
 YMVVVSRLCLLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNIINHFYCDNVPLLALSCSDTYLPE  
 TVVFISAATNVVGSLLIIVLSYFNIVLSILKICSSEGRKKAFSTCASHMMAVTIFYGTLLFMVYQP  
 45 RSNHSLDTDDKMASVFYTLVIPMLNPLIYSLRNKDVKLTALQRFMTNLCYSFKTM (SEQ ID NO:  
 133)

50 ATGGCTCCTGAAAATTTACCCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC  
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG  
 GAACCTGGGCATCATCACCTCACAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT  
 TCCTGCAACATCTGGCTCTCATTAATCTTGGTAACTCTACTGTCATTGCCCCATAAATGCTG  
 ATTAACTTTTTAGTAAAGAAGAAAACCTCATTCTATGAATGTGCCACCAACTGGGAG  
 GGTCTTGTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT  
 GTGGCTATTTGTAACCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCTCCTGCT  
 55 GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCACTTATGTATTCT  
 CTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTTACTGTGATAATGTTCTCTGTTA  
 GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA

ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA  
 AAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG  
 CAGTCACAATTTTTATGGGACATTGCTATTCATGTATGTGCAGCCCCGAAGTAACCATTC  
 ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT  
 5 CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA  
 AATCTGTGCTATTCTTTAAAACAATGTAA (SEQ ID NO: 134)

#### AOLFR73 sequences:

MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFGFLIHYLVTVIGNLGMVILTYLDSKLHTP  
 10 MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIISELFILSAMAYDRYV  
 AICKPLLYVIIMAEKVLWVLVIVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT  
 NELELILIFSGCNLLFSLIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL  
 QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

15 ATGAATCATGTGGTAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA  
 TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTGGACTCTTCCTCATCATATA  
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA  
 CACACCCCCATGTACTTTTCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT  
 CATTGCCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG  
 20 TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC  
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA  
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT  
 TCTCACAATTAAGTTATTTAACTGTCTTCTGTGGCTCAAACATAATCAGCTATTTTTACT  
 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT  
 25 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT  
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC  
 TGTAAGTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACCTGCA  
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCTGTTG  
 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAGATGCTCTAA  
 30 AGAGAACTTTAACCAATCGATTCAAAATCCCATTTAA (SEQ ID NO: 136)

#### AOLFR74 sequences:

MEQHNLTTVNEFILTGITDIAELQAPLFAFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH  
 LAFMDLGYSTTVGPKMLVNFVVDKNIISYFYCATQLAFFLVFIGSELFILSAMSVDLYVAICNPL  
 35 LYTVMSRRVCQVLVAIPYLYCTFISLLVTIKIFTLSCGYNVISHFYCDLPLPLLCNTHIEILI  
 ILIFAAIDLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMVYQPKSSH  
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC  
 40 GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG  
 GCAATTTGGGCATGATTGTCCTACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTACTT  
 TTTTCTCAGACATCTGGCTTTTCATGGATCTTGGTTATTCAACAACGTGTTGGACCCAAAATG  
 TTAGTAAATTTTGTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC  
 TTTCTTTCTGTGTTCAATTGGTAGTGAACCTTTTATTCTCTCAGCCATGTCTACGACCTCT  
 45 ATGTGGCCATCTGTAACCCCTCTGCTATACACAGTAATCATGTGCAGGAAGGTATGTCAGGT  
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCATTTCTTCTTAGTCACCATAAAGATTT  
 TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTTG  
 TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT  
 TGATTTGATTTTCATCTCTTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT  
 50 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTTCTACCTGTGGAGCCACCTGACAGTG  
 GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCCCT  
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCATGTTGAATCCCTTGA  
 TCTATAGTTTACGAAACAAAGATGTAAATATGCCCTACGAAGGACATGGAATAACTTATG  
 TAATATTTTTGTTTAA (SEQ ID NO: 138)

55

**AOLFR75 sequences:**

MEGKNQTNISEFLLLGFSWQQQQVLLFALFLCLYLTLGLFGNLLILLAIGSDHCLHTPMYFFLA  
 NLSLVDLCPLSATVPKMLLNQITQTISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI  
 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMHLHFCSDNVIIHFFCDINSLPLSCSD  
 5 TSLNQLSVLATVGLIFVPSVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT  
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFYSLRNNEKLGTLKKTLSRPGAVAHACNPSTL  
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

10 ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC  
 AACAAACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTTAACAGGGCTGTTTGGGA  
 AACTTACTCATCTTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCCATGTATTCTT  
 CCTTGCCAATCTGTCCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC  
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT  
 CTGTATGATGTTTGCCAATATGGACAATTTTCTTCTCACAGTGATGGCATATGACCGTTAC  
 15 GTGGCCATCTGTACCCCTTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT  
 GGTAGCTGCACCTTGGGTCAATGCCATTTTGAACCCCTCTCTTGACACTCTTATGATGGCCC  
 ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTCTTCTGTGATATCAACTCTCTCCTC  
 CCTCTGTCTGTTCGACACCAGTCTTAATCAGTTGAGTGTTCTGGCTACGGTGGGGCTGA  
 TCTTTGTGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG  
 20 AAAGTCCCTTCTGCCCCAAGGAAACTCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCTT  
 GGTCATTCTTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCTTATCCAATCACTCT  
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTTATGGTTGTAGCACCTGTGTTGAATCCAT  
 TCATTTACAGTTTAAAGAAACAATGAAGTGAAGGGGACTTTAAAAAGACCCTAAGCCGGC  
 CGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA  
 25 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

**AOLFR76 sequences:**

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMIIILLDSHLHTPMYFFLSNLSLA  
 GIGYSSAVTPKVLTLGLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY  
 30 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL  
 VLISFNVFFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM  
 DTDKIASVFYTMIPMLSPIVYTLRNKDVKNFAMKVVEKAKYSLDSVF (SEQ ID NO: 141)

35 ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA  
 CTACAGGTTCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT  
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTTCTCA  
 GTAACCTGTCTCTTGCAAGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTTAACTGG  
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCTGTGCTGCTCAGATGTTCTTTTGT  
 GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGCTCAATGGCCTATGACCGCTACGCAG  
 40 CAGTGTGTAACCCCTACATTATACCACCACATGACAACACGTGTGTGTGCTGTCTGGC  
 TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTCGCC  
 TCTCTTTTGCATGTCCAATGTGATTCATCACTTTTTCTGTGACAAACCAGCAGTCATTACT  
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTCTTATATCAAGTTTTAATGT  
 CTTTTTGCACCTCTTGTTACCTTGATTTCTATCTGTTTATATGATCACCATTCTTAAGAG  
 45 GCACACAGGTAAGGGATACCAGAAGCCTTATCTACCTGTGGTTCTCACCTCATTGCCATT  
 TTCTTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTCCAGTCATTCCATGGA  
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCATGCTCAGTCTATAGTCT  
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTCATGAAGGTTGTTGAGAAGGCAAAAT  
 ATTCTCTAGATTCACTCTTTTAA (SEQ ID NO: 142)

50

**AOLFR77 sequences:**

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS  
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTMGVAEGVLLVMSYDRYVAVC  
 QPLQYPVLMRRQVCLLMGSSWVVGVLNASIQTSITLHFPYCASRIVDHFFCEVPALLKLSA  
 55 DTCA YEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGIFYGA

AVFMYMVPcAYHSPQQDNVVSFLFYSLVTPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC  
(SEQ ID NO: 143)

5 ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT  
CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTCAATGTTTGTATAGGCCTTCTGGGC  
AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTAATCTCT  
GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA  
TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCTATGGAGGTGGTGCAGCTCAAATATTCT  
10 TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCTCATGTCTTATGACCGTTA  
TGTTGTCTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGTCTG  
ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACCC  
TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA  
CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC  
TGATCCTAATGCTCCCTCTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGTGTT  
15 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTCACCACTGCTCCTCGCACATCA  
CGGTAGTGGGGCTCTTTTATGGTGCCGCCGTGTTTATGTACATGGTGCCTTGCCTACCA  
CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTACCCCTACACTCAAC  
CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTGGTCAAAGTGCTTAGCA  
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

20

**AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVFLVYLLNLTGNVLIVGVVRADTRLQTPMYF  
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH  
PLRYPLLMGAVCFRVALACWVGGLVPVLGPTVAVALLPFCQKQGAUVVQHFFCDSGPLRLRLAC  
25 TNKKLEETDFVLASLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI  
FLYVRPSQSGSVDTNWAVTVITTFVITPLNPFYIALRNEQVKEALKDMFRKVVAGVLGNLLLD  
KCLSEKAVK (SEQ ID NO: 145)

30 ATGAGTCCTGATGGGAACCACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA  
AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT  
GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT  
GTACTTCTTTCTGGGTAACTGTCTGCCTAGAGATACTGCTCACTTCTGTATCATTTCCAA  
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCCCTTGTGTCATGTATCACCCA  
ATTCTATTTCTACTTCTTCTCGGGGCCTCCGAGTTCTTACTGTTGGCTGTATGCTGTGCGG  
35 ATCGCTACCTGGCCATCTGTATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG  
CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGGGACTCGTCCCTGTGCTTGGTCCCACAGTG  
GCTGTGGCCTTGCTTCCCTTCTGTAAGCAGGGTCTGTGGTACAGCACTTCTTCTGCGACA  
GTGGCCCACTGCTCCGCTGGCTTGCACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT  
CCTGGCCTCCCTCGTCATTGTATCTTCTTCTGCTGATCACTGCTGTGCTCCTACGGCCTCATTG  
40 TGCTGGCAGTCTGAGCATCCCCCTCTGCTTACAGCCGTCAGAAGGCCTTCTCTACCTGTAC  
CTCCCACTTGATAGTGGTGACCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT  
CGCAGAGTGGTTCTGTGGACACTAACTGGGCAGTGACAGTAATAACGACATTTGTGACAC  
CACTGTTGAATCCATTCTATGCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA  
CATGTTTAGGAAGGTAGTGGCAGGCGTTTATAGGAATCTTTTACTTGATAAATGTCTCAGT  
45 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

**AOLFR79 sequences:**

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMALIFTDSLQSP  
MYFFLNVLVSFLDICYSSVTPKLLVNFLVSDKSISFEGCVVQLAFFVVHVTAESFLLASMAFYDR  
50 FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSIAQTGNVFALPFCGPNQLTHYYCDIPPLH  
LACANTATARVVLVVSALVTLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI  
FYGTVVFTYVQPHGSTNNTNGQVVSFYTIIIPMLNPFYISLRNKEVKGALQRKLQVNIFFG  
(SEQ ID NO: 147)

55 ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCACACCCAGTCACCAAGTTCATCT  
TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGAGCCATCCTGCTCAT



CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT  
 CTCCAAAGCCCAATGTATTTCTTCTCAATGTCTCTCGTTTCTTGATATTTGTTACTCTTCT  
 GTGGTCACACCTAAGCTCTTGGTCAACTTCTGGTCTCTGACAAGTCCATCTCTTTTGGG  
 GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCTGCTGGC  
 5 CTCCATGGCCTATGACCGCTTCTTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA  
 CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCTATGCATTTGGTGGAGCCAACCTCCGC  
 TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCCAACAGCTAACACACTAC  
 TACTGTGACATAACACCCCTTCTCCACCTGGCTGTGCCAACACAGCCACAGCAAGAGTGG  
 TCCTCTATGTCTTTTCTGCTCTGGTCAACCCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT  
 10 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT  
 CCACTTGTGCCTCCCACTTTCTGGCCATTGCCATTTTCTATGGCACTGTGGTTTTCACCTAT  
 GTTCAGCCCCATGGATCTACTAACAATACCAATGGCCAAGTAGTGTCCGCTCTTCTACACCA  
 TCATAATTCCCATGCTCAATCCCTTCATCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC  
 TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

15

**AOLFR80 sequences:**

MEGINKTAKMQFFRPFSPDPEVQMLIFVVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA  
 NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLVVMAYDRFIAICH  
 PLRYRLIMSWSLCVELLVGSVLGFLSLPLTILIFHLPFCHNDEIYHFYCDMPAVMRLACADTR  
 20 VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQQAYSTCSSHILVLLQYGCTSFYLSPS  
 SSSPEMGRVVSVAAYTFITPILNPLIYSLRNKELKDALRKALRKF (SEQ ID NO: 149)

ATGGAAGGAATAAATAAACTGCAAAGATGCAGTTTTTCTTTCTGTCATTCTCACCTGACC  
 CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCTGATGATGTATCTGACCAGCCTCGGTGG  
 25 AAATGCTACAATTGCAGTCATTGTTTCAATCAATCCCTCCACACCCCCATGTACTTTT  
 TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATTTGGCCTTG  
 GCAAACCTCCTTTCAATGGGCAAACTCCTGTTTCCATCACGGGATGTGGCAGCCAGATGT  
 TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCTGCTGGTAGTCATGGCTTATGACCGG  
 TTTATAGCGATCTGTCAACCTCTGCGATACAGGCTCATCATGAGCTGGTCTTGTGTGG  
 30 AGCTGCTGGTAGGCTCCTTGGTGTGGGGTCTCCTGTTGTCAGTGGCACTCACCATTTTAATC  
 TTCCATCTCCCATTTCTGCCACAATGATGAGATCTACCACTTCTACTGTGACATGCCTGCAGT  
 CATGCGCCTGGCTTGTGCAGACACACGCGTTCAACAAGACTGCTCTGTATATCATCAGCTTC  
 ATCGTCCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT  
 TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC  
 35 TTAGTGGTCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCAGTTCAGCTA  
 CTCTCCTGAGATGGGCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC  
 CCCTTGATCTATAGTTTGAGGAACAAGGAAGTGAAGATGCCCTAAGGAAAGCATTGAGA  
 AAATTCTAG (SEQ ID NO: 150)

40 **AOLFR81 sequences:**

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIIRLNRLHTPMYFFLSS  
 LSFLDFCYSSVITPKMMKLWMESHLIVPETRPSRMMSNQTLVTEFILQGFSEHPEYRVFLSCF  
 LFLYSGALTGNVLITLITFNPGLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC  
 MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTH  
 45 TGLMLRLDFCGPNVHHFFCEVPPLLLSLSSTYVNGVMIVLADAFYGVNFMITIASYGFIVSSI  
 LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL  
 IYTLRNKEVKAALRKLFPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG  
 50 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT  
 ACCGGGTGTTCTTATTCAGCTGTTTCTTCTTCTACTCTGGGGCCCTCACAGGTAATGTC  
 CTCATCACCTTGGCCATCACGTTCAACCCCTGGGCTCCACGCTCCTATGTACTTTTCTTACT  
 CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGCTGGCCAGT  
 CTGGTGTGCGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCAGCTCTATTTCTCA  
 55 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTTCATGGCCTATGACCGGTACGCAGC  
 CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC

ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT  
 TGGATTTCTGTGGCCCAATGTCATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT  
 CTCTCTGCAGCTCCACCTACGTCAACGGTGTGATGATTGTCTTGGCGGATGCTTTCTACG  
 GCATAGTGAACCTTCTGATGACCATCGCGTCCTATGGCTTCATCGTCTCCAGCATCCTGAA  
 5 GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTCACCGTG  
 GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG  
 CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCCTACCCTCAACCCCT  
 CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTTCTTC  
 AGAAATTAA (SEQ ID NO: 152)

10

**AOLFR82 sequences:**

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIISVKASQALKNPMFFFLFYLSL  
 SDTCLSTSIAPRMIVDALLKKTISFSECMIQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII  
 SQWVCGVLMMAVAWVGSCVHSLVQIFLALSPLFCGPNVINHCFCDLQPLLKQACSETYVVNLLL  
 15 VNSNGAICAVSYVMLIFSIVIFLHSLRNHSAEVIKKALSTCVSHIIVILFFGPCIFMYTCPATVFP  
 MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT  
 GGAAGAAAATAGTGTGTTATTTTTTGGCTCTCTACTTGGGAACACTGTTGGGTAAATTT  
 20 GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTTCTT  
 TTCTACTTATCTTTATCTGATACTTGCCCTCTCTACTTCCATAGCCCCTAGAATGATTGTGGA  
 TGCCCTTTTGAAGAAGACAACATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC  
 CATGTCCTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA  
 CATCTGTAAGCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTGATG  
 25 GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGGCCTGAGTTT  
 GCCATTCTGTGGCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTTGTGAAA  
 CAAGCCTGTTCAAGAACCTATGTGGTTAACCTACTCCTGTTTCCAATAGTGGGGCCATTT  
 GTGCAGTGAGTTATGTCATGCTAATATCTCCTATGTCATCTTCTTGCACTTCTCTGAGAAAC  
 CACAGTGCTGAAGTGATAAAGAAAGCACTTTCACATGTGTCTCCACATCATTGTGGTCA  
 30 TCTGTCTTGGACCTTGCAATTTATGTACACATGCCCTGCAACCGTATCCCCATGGAT  
 AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTTCTCAACCCTGTGATTTACACGCT  
 GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA  
 TGACAAAAGATAA (SEQ ID NO: 154)

**AOLFR83 sequences:**

MGNWTAAVTEFVLLGFSLSRVELLLLVLPLTFLLTLLGNLLIISTVLSCSRLHTPMYFFLCNL  
 SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLLTVMYSYDRYATICPLRYT  
 TIMRPSVCIGTVVFSWVGGLSVLFPTILISQLPFCGNSNIINHFFCDSGPLLALACADTTAIELMDF  
 MLSSMVLCCIVLVAYSITYIILTIVRIPSASGRKKAFNTCASHLTIVIIPSGITVFYIVTPSQKEYL  
 40 EINKIPLVLSSVTPFLNPFYITLRNDTVQGVLRDVWVRVRGVFEKRMRAVLRSRLSSNKDHQ  
 GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

ATGGGTAACCTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG  
 AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCCACGTTCTGCTGACTCTTCTGGGGAA  
 45 CCTGCTCATCATCTCCACTGTGCTGCTCCTGCTCCCGCCTCCACACCCCATGTACTTCTTCT  
 TGTGCAACCTCTCTATCCTGGACATCCTCTTACCTCAGTCATCTCTCCAAAAGTGTGGCC  
 AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT  
 ACTTTTCTTGGGCACAGTTGAGTTCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC  
 ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG  
 50 TTGTATTCTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCCAG  
 CTGCCCTTCTGTGGCTCCAATATCATTAACCACTTCTCTGTGACAGTGGACCCTTGCTGGC  
 CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC  
 ATCCTCTGCTGCATAGTCTCGTGGCCTATTCTATACGTACATCATCTGACCATAGTGCG  
 CATTCTTCTGCAAGTGGAAGGAAGAAGGCCTTTAATACCTGTGCTTCCCACCTGACCATA  
 55 GTCATCATTCCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCCAGAAAGAATATCT  
 GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGAAGTCCATTCTCAACCCCTTT



ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCCTCAGGGATGTGTGGGTCAGGGTT  
CGAGGAGTTTTTGAAGAGGATGAGGGCAGTGCTGAGAAGCAGATTATCCTCCAACAAA  
GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGT  
AG (SEQ ID NO: 156)

5

**AOLFR85 sequences:**

MGAKNNVTEFVLFGLFESREMQHTCFVVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL  
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY  
TAIMDCRKCGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV  
10 GLIVVANSGLMISLASFILISYVILLNLRSSQSEDRRKA VSTCGSHVITVLLVLMPPPMFYIRPS  
TTLAADKLIILFNIVMPPLLNLPLIYTLRNNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

ATGGGTGCCAAGAACAATGTGACTGAGTTTGTATTATTTGGCCTTTTTGAGAGCAGAGAGA  
TGCAGCATACATGCTTTGTGGTATTCTTCCTCTTTCATGTGCTCACTGTCTGGGGAACCTT  
15 CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCCTGA  
GCCAGTTGTCTTTTGCTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC  
ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTCTGCCCA  
CTTCTTTGGTGGCACTGAGATCTTCCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC  
ATCTGTAGGCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG  
20 GGGCCTCCTGGTTAGCTGGCTTCCTGCATTCCATCCTGCAGACCCTCCTCACGGTTCAGCTG  
CCTTTTGTGGGCCCAATGAGATAGACAACCTTCTTCTGTGATGTTTCATCCCTGCTCAAGTT  
GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTCTT  
TTAGCATCCTTTTTATCCTTATCATTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA  
GTCATCTGAGGACCGGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCTT  
25 TTGGTTCTCATGCCCCCATGTTTCATGTATGATGCCACCTTTGCTGAACCTTTGATCTATACACTAA  
ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCTTTGATCTATACACTAA  
GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG  
AGAAGTGA (SEQ ID NO: 158)

**AOLFR86 sequences:**

MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVVFLLIYVTV  
GNMLIVVTTSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF  
LGGVEILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAVLGGFLHSLVQLLLVLWLPFC  
GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRC  
35 KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR  
KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT  
CTCAGTGACCTTGGAATCTATGGACATACCACAAAATATCACAGAATTTTCATGCTGGGG  
40 CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTTGCTGATCTATGTGG  
TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACTCCAGCCCCACGCTGGCTTC  
CCCTGTGATTTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC  
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG  
GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG  
45 CTTATGACCGCTATGTGGCCATCTGTAAGCCCCTGCACAATACTACCATCATGACCAGGCA  
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGCATTATTGGTTTCA  
CTCCTCCTGGTCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCCTGTGA  
CTTGTAACCTTTGCTGGAAGTTGCCTGCACCAATACGTATGTCAATTGGTCTGCTGGTGGTT  
GCCAACAGTGGTTAATCTGCCTGTTGAACCTCCTCATGCTGGCTGCCTCCTACATTGTCAT  
50 CCTGTACTCCTTGAGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA  
GCCCACTTCAATTGTTGTTGCCCTTGTCTTTGTGCCCTGTATATTTACTTATGTGCATCCATTT  
TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA  
TCCACTCATTTATACCCTGAGAAATGAAGAGGTAATAAATGCCATGAGAAAGCTCTTTACA  
TGGTAA (SEQ ID NO: 160)

55

**AOLFR87 sequences:**

MNNAQLSLGFIDLGPSVLQKILTKIILLFKMYVSNCPCAIHRKINYPNTKLDSEQVNNITEFI  
 LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIVVTITTSPLDSPVYFFLSFFSIDGCSSTMAP  
 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEILLVVMAYDCYVAICKPLYLITMNRQVCGL  
 5 LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLLKLSCTDTHVGLFVAANSGLM  
 CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFVPCILVYLRPMITFPIDKAVSVFYTVVTPM  
 LNPLIYTLRNTEVKNAMKQLWSQIIWGNLDC (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC  
 10 AGAAAATAATCCTGACCAAAATTATTTATTGTTCAAAATGTATGTGTCAAATTGCAATCC  
 TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAATCGGATTCGAGCAAGTGAAC  
 AACATAACGGAATTCATCTTGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT  
 TTGCTGTGTTTAACTCATCTACTTTCTCACCATTGGTAGACAACCTAATCATTGTGGTGACA  
 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGATTTTTTCTGTCTTTCTTTCTCTTCAT  
 15 AGATGGCTGCTCCTCTTCTACCATGGCCCCAAAATGATATTTGACTTACTCACTGAAAAG  
 AAAACTATTTCTTTCAGTGGGTGCATGACCCAGCTCTTGTAGAACATTTCTTTGGGGGAG  
 TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCT  
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTC  
 GGGGGATTCTTACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC  
 20 CAATGTCAATTGACCATTTCTATCTGTGACCTTTTCCCTCTGCTAAACTCTCCTGCACTGACA  
 CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT  
 ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTACCTGCGC  
 CTTCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA  
 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTATACTGTGGTAACACCCATGTTA  
 25 AACCCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG  
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

**AOLFR88 sequences:**

MWQKNQTSADFILEGLFDDSLTHLFLFSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ  
 30 LSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH  
 PLRYAVLMNKKVGLMMAVMSWLGA SVNSLIHMAILMHFPFCGPRKVYHFYCEP AVVKLVLC  
 GDITVYETTVYISSILLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS  
 YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRRDVITQCIQRLQLWLP  
 RV (SEQ ID NO: 163)

ATGTGGCAGAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT  
 CCCTTACCCACCTTTTCCTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC  
 AACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT  
 40 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT  
 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC  
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCATGTCCTATGACCGCTAT  
 GTTGCCATCTGTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA  
 TGGCTGTCTATGTCATGGTTGGGGGCATCCGTGAACCTCCCTAATTCACATGGCGATCTTGAT  
 GCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCCAGCTGTTG  
 45 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT  
 CCTCTCCTCCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATCA  
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCTCCACCTCACGGTG  
 GTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGGTCCCAGTGCATCT  
 ATTGACAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCACATTGAATTCTCTG  
 50 ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGTGAGGAGAGAT  
 GTTATACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:  
 164)

**AOLFR89 sequences:**

MLDPSISSHTLYLHSLFPQGLRKGTMWQKNQTSADFILEGLFDDSLTHLFLFSLTMVVFLIAVS  
 55 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYL

CLGGAECFLLA VMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWL GASVNSLIHMAILMHF  
PFCGPRKVYHFYCEFPVAVKLVCGDITVYETTVYISSILLLLPIFLISTS YVFILQSVIQMRSSGSK  
RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA  
KALRRVLRDVTQCIQRLQLWLPRV (SEQ ID NO: 165)

5

ATGCTGGACCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT  
GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG  
GCTCTTCGATGACTCCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCCTTAT  
TGCGGTGAGTGGCAACACCCCTACCATTTCTCCTCATCTGCATTGATCCCCAGCTTCATACA  
10 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT  
CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA  
ACCCAGCACTTCTCTATTTGTGTCTAGGTGGTGGCTGAATGTTTTCTCTTAGCTGTCTATGTC  
CTATGACCGCTATGTTGCCATCTGTCTACCTGCGCTATGCTGTGCTCATGAACAAGAAG  
GTGGGACTGATGATGGCTGTCTATGTCATGGTTGGGGGCATCCGTGAACTCCCTAATTCACA  
15 TGGCGACTCTTGATGCACCTCCCTTTCTGTGGGCCTCGAAAGTCTACCACTTCTACTGTGA  
GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC  
ATCAGCAGCATTCTCCTCCTCCTCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTT  
CAAAGTGTCAATCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT  
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG  
20 TCCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA  
CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT  
GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG  
TAG (SEQ ID NO: 166)

#### 25 AOLFR90 sequences:

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF  
VLLGLSQNPVQEIFVVFVFLVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI  
TPKMIVDSL YVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRR  
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMDLYPLLELACTDTHIFGLMVVNSG  
30 FICINFSLLLVS YAVILLSLRTHSSEGRWKALSTCGSHLAVVILFFVPCIFVYTRPPSAFSLDKMA  
AIFYILNPLL NPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACCTGGATGTACCAACTTGTTAA  
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCTTTGTCCTAATTGCAGACTATA  
35 CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA  
ACTGAGTTTGTCTCCTGGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG  
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCACTTCTC  
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTCTCCTGGA  
TGCGTGCTTCTCATCTGTCATACCCCAAGATGATTGTAGACTCCCTCTATGTGACAAAA  
40 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTGTGCTGAACACTTCTTTGCTGGGGTGG  
AGGTGATTGTCTCCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA  
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG  
GGCCTCTTGCAATCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA  
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC  
45 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG  
TTGCTTGTCTCCTATGCTGTCATCTTGCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG  
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA  
TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT  
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC  
50 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA  
AACTTTAA (SEQ ID NO: 168)

#### AOLFR91 sequences:

MGNWSTVTEITLIAFPALLEIRISLFFVLVVTYTLTATGNITIISLIWIDHRLQTPMYFFLSNLSFL  
55 DILYTTVITPKLLACLLGEEKTISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI  
MNSRACLLLVLGCWVGAFSLVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFL

SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD  
YDKVAAVLITVVTPLLNPFYISLRNEKVQEVLRQETVNRIMTLIQRKT (SEQ ID NO: 169)

ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA  
5 TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT  
CACCATCATCTCCCTGATATGGATTGATCATCGCTGCAAACCTCCAATGTACTTCTCCTCA  
GTAATTTGTCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC  
CTCCTAGGAGAAGAGAAAACCATATCTTTGCTGGTTGCATGATCCAAACATATTTCTACT  
10 TCTTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCCTTTGACCGCTACATGGC  
TATCTGCGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT  
CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTTGTTTCCAACCATTTAGTGACAAGGC  
TACCTTACTGTAGGAAAGAAATTAATCATTTCTTCTGTGACATTGCCCTCTTCTTCAGGTG  
GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTATCCT  
GAGCTCCCTGGCATTCACTACTGGGTCCTACGTGTACATAATTTCTACCATCCTGCGTATCC  
15 CCTCCACCCAGGGCCGTCAGAAAGCTTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC  
ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT  
ATGACAAGGTGGCCGCTGTCCTCATCAGTGGTGACCCCTCTCCTGAACCCCTTTTATCTA  
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTTGAGAGAGACAGTGAACAGAATCATGAC  
CTTGATACAAAGGAAAACCTGA (SEQ ID NO: 170)

20

**AOLFR92 sequences:**

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLTYILTLAGNGLIATVWAEPRLOIPMYFFLCNLSFLE  
IWYTTTTVPKLLGTFVARTVICMSCLLQAFFHFFVGTTEFLILTIMSFDRLTICNPLHPTIM  
TSKLCLQLALSSWVVGFTIVFCQTMILLQLPFCGNNVISHFYCDVGP SLKAACIDTSILELLGVIA  
25 TILVIPGSLLFNMISYIYLSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK  
INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC  
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCCTTGCAAGGCAATGGG  
30 CTTATTATTGCCACTGTGTGGGCTGAGCCCAGGCTACAAATCCAATGTACTTCTTCCTTTG  
TAACTTGTCTTTCTTAGAAATCTGGTACACCACACAGTCATCCCCAACTGCTAGGAAC  
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCTGCTGCCTGCTGCAGGCCTTCTTCCACT  
TCTTCGTGGGCACCAACCGAGTTCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC  
ATCTGCAATCCCCCTCACCAACCCACCATCATGACCAGCAAACCTCTGCCTGCAGCTGGCCC  
35 TGAGCTCCTGGGTGGTGGGCTTACCAATTGTCTTTTGTGACGATGCTGCTCATCCAGTT  
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCCAGTTTGAAA  
GCCGCCTGCATAGACACCAGCATTTTGGAACCTCGGGCGTCATAGCAACCATCCTTGTA  
TCCCAGGGTCACTTCTCTTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA  
ATTCTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT  
40 CTCCCTGCTCTACGGGGCTGTTCTGTTTCATGTACCTAAGACCCACAGCACACTCCTCCTTTA  
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCTTCTGAATCCCTTTATT  
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG  
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

45 **AOLFR93 sequences:**

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL  
SALEILVTIIVPVMLWGLLLPGMQTIYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN  
PLRYNIIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLKLSCN  
NTLFTEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY  
50 VKPKQTQAADYNWVSLMVSVVTPFLNPFIFTLRNDKVIEALRDGVKRCCQLFRN (SEQ ID  
NO: 173)

ATGTTGATGAATTAATCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA  
ACTACATCATATCCTTTTGTCTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA  
55 CAGTCATCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGATTTCTTCTC  
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCGTGATGCTTTGGG

GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG  
 TACCTTGCTGTGGGGACAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG  
 TGGCTGTCTGTAACCCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT  
 5 GGTTCTTGTGTGTCATGGGTGTTTGGGTTTCTTTTTCAAATCTGGCCGGTCTATGTCATGTTTC  
 AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT  
 CAAACTATCCTGCAATAATACTCTTTTACGGAGTTTATCCTCTTCTTAATGGCTGTTTTTG  
 TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTCTC  
 AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG  
 TGTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACGCAGGCA  
 10 GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTTCAGTAGTAACTCCTTCTCAATCCTTT  
 CATCTTACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC  
 TGCAACTATTGAGGAATTAG (SEQ ID NO: 174)

**AOLFR94 sequences:**

15 METWVNQSYTDGFFLLGIFSHSTADLVLFVSVMVAVFTVALCGNVLLIFLIYMDPHLHTPMYFF  
 LSQSLMDLMLVCTNVPKMAANFLSGRKSISFVCGIQLFVCLVGSEGLLLGLMAYDRYVA  
 ISHPLHYPILMNQVRVCLQITGSSWAFGIIDGLIQMVVMNFPYCGLRKVNHFCEMLSLLKLAC  
 VDTSLFEKVIFACCVFMLLPFSIIVASYAHILGTVLQMHSQAQWKKALATCSSHLTAVTLFYG  
 AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH  
 20 (SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAGTCCTACACAGATGGCTTCTTCCTCTTAGGCATCTTCTCCC  
 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT  
 GGAATGTCTCCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCCATGTACTT  
 25 CTTCCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG  
 GCAGCCAACTTCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATTG  
 GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGTGGGACTCATGGCTTATGACCG  
 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC  
 AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT  
 30 AATGAATTTCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC  
 TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGCTGTG  
 TCTTCATGCTTCTCTTCCCATCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT  
 GTGCTGCAAATGCACTCTGCTCAGGCCTGAAAAAGGCCCTGGCCACCTGCTCCTCCACCC  
 TGACAGCTGTCACCCCTCTTCTATGGGGCAGCCATGTTTCTACCTGAGGCCTAGGCACTA  
 35 CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCCTTACTCCCATGCTC  
 AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG  
 GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

**AOLFR95 sequences:**

40 MLGSKPRVHLYILPCASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL  
 GNVGMMTIMTDPRLNTPMYFFLGNSFIDLFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA  
 LLIVTEGFLAAMAYDRFIAICNPLLYSVQMSTRCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS  
 RAVDHFYCDRLPLQRLSCSDLFIHRMISFSLSCHILPTIIVIVSYMYIVSTVLKIHSTEGHKKAFST  
 CSSHLGVVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE  
 45 KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGGCCTGTGCCTCTCAACAGGTTTC  
 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCACTTCTTGCAGG  
 CTTCAGGGTACGCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTTGTTTGTATGCCA  
 50 TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC  
 ACCAATGTATTTTTCTTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCTGTTATTGA  
 ACCCAAGGCTATGATCAACTTCTGGTCTGAAAAACAAGTCTATCTCCTTTGCAGGCTGTGTG  
 GCCAGCTCTTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTTCTCCTGGCGGCCATGGC  
 TTATGACCGCTTTATTGCCATCTGCAACCTCTGCTCTACTCTGTTCAAATGTCCACACGTC  
 55 TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTTGTGGCTGCATTAGCTCAGTTATTCAGACT  
 AGCATGACATTTACTTTATCTTTTTGCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC

TCGCCCCACTTCAGAGACTGTCTTGTTCTGATCTCTTTATCCATAGAATGATATCTTTTTCTCT  
TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG  
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT  
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTCTTTTTATGTATCTCACTCCTGAC  
5 AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA  
ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA  
GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

**AOLFR96 sequences:**

10 MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAITYVTLLGNFLIVTVTSVDLALQTPMYFFLQN  
LSLLEVCFTLVMVPKMLVDLVSPRKIISFVGCQTQMYFFFFGSSECFLLSMAYDRFVAICNP  
LHYSVIMNRSCLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNVDFHFFCDGPPVLKLVTV  
DTTMYEMQALASTLLFIMFPFCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL  
TYLRPKSNQSPESKLVSLSYTVITPMLNPIHYGLRNNEVKGAVKRTITQKVLQKLDVF (SEQ  
15 ID NO: 179)

ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC  
CCGAGATGCAAGTTTCCCTCTTTATTTTTTCTGGCCATTTATACAGTCACTTTGTTGGGC  
AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT  
20 TCTTCAAAATCTGTCACTTCTTGAAGTATGTTTCACTTGGTTATGGTGCCAAAAATGCTTG  
TAGTCTAGTGTCCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCAGATGTACTT  
CTTCTTCTTCTTGGCAGTTCTGAATGTTTCCTTCTCTCCATGATGGCTTATGATCGCTTTGT  
GGCCATCTGTAACCCCTCTCCATTATTCAAGTCATAATGAACAGGTCCCTATGCTTGTGGATG  
GCCATAGGCTCTTGGATGTCCGGTGTCTCTGTGTCTATGCTACAGACAGCTTGGATGATGG  
25 CCTTCTCTTCTGTGGACCAAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCCAGTGTTA  
AAACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT  
TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCATTATCATAACAATTCTG  
AGGATGTCTCTGTCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT  
GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAATCAAACCAGTCC  
30 CCTGAGAGCAAGAAGCTAGTGTCAATTGTCCTACACTGTCATCACACCTATGCTAAACCCCA  
TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAA  
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

**AOLFR97 sequences:**

35 MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSFMVVPSFSIAEHWRRMKGANLSQGMFEFL  
LGLTTDPQLQRLLFVFLGMYTATLLGNLVMFLLHVSATLHTPMYSLKLSLDFCYSSSTV  
PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLAAMAYDRYAICNPLLYSTIMSPEVC  
ASLIVGSYSAGFLNSLIHTGCIIFSLKFCGAHVVTFFCDGPPILSLSCVDTSICEILLFIFAGFNLLS  
CTLTILISYFLILNTILKMSSAQGRFKAFTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRIVA  
40 VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAAGGCTGT  
CCTTAGGCAGAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC  
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT  
45 GGAGTTTGAGCTCTTGGGCCTCACCCTGACCCCACTCCAGAGGCTGCTCTTCGTGGTG  
TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCTCTGATCCATG  
TGAGTGCCACCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGGAATTC  
TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGTGTAACCTTCTTGGCCAAGAGGAAAGTGA  
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTTATGCGGGTTTGGCCACCACTGATGC  
50 TATCTCATCGCTGCCATGGCCTATGACCCTATGCCGCTATTGTAAACCCCTGCTCTACTC  
AACCATCATGTCTCCTGAGGTCTGTGCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC  
CTCAATTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTGCT  
CACTCACTTCTTCTGTGATGGGCCACCCATCCTGTCTTGTCTTGTGTAGACACCTCACTGT  
GTGAGATCCTGCTCTTCAATTTTGTGTTTCAACCTTTTGTGCTGCACCCCTACCATCTTG  
55 ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAAATGAGCTCGGCCCAAGGAGGTTTA  
AGGCATTTTCCACCTGTGCATCCCACCTCACTGCCATCTGCCTCTTCTTGGCACAACACTT

TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA  
TCTACACAGTGGTGATCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT  
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

5 **AOLFR98 sequences:**

MRGFNKTTVVVTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLLFI  
LSFSESCYTFVIIPQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLLAVMGYDRYVAICHPLR  
YTLINKRLGLELISLSGATGFFIALVATNLICDMRFGPNRVNHYFCDMAPVIKLACTDTHVKE  
LALFSLSILVIMVPFLLILISYGFIIVNTILKIPSAEGKKAFTVCASHLTVVFVHYGCASIIYLRPKSK  
10 SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC  
TGGGGGAGCTCCAGCTGCTGCTTTTGTGTCATCTTCTCTCTATACTTGACAATCCTGGTG  
GCCAATGTGACCATCATGGCCGTTATTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG  
15 GCTTTCTATTTCATCCTTTTCATTTTCTGAGTCTGCTACACTTTTGTGTCATATCCCTCAGCTGC  
TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT  
CTTTTCTCTGGCTTTGCTTGACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT  
ATGTAGCAATTTGTCAACCCTCTGAGGTACACACTCATCATAAACAAGGCTGGGGTTGGA  
GTTGATTTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT  
20 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTTCTGTGACATGGCACCTGT  
TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTTAGCCTCAGCATC  
CTGGAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACCCAT  
CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTACCTGTGCCTCACATCTCACT  
GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC  
25 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT  
CTTGTCTACAGTCTGAGGAACAAAGAGGTAAAACTGCATTGAAAAGAGTTCTTGGAATG  
CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

**AOLFR99 sequences:**

30 MERVNETVVREVIFLGFSSLARLQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHIPMYFFLAILSC  
SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV  
LMGHGVCMLVAAACACGFTVAQIITSLVFHLPFYSSNQLHHFFCDIAPVLKLASHHNHFSQIV  
IFMLCTLVLAIPLLILVSYVHLSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFYLRPQSNY  
SSSQDALISVSYTIITPLFNPMIYSLRNKEFKSALCKIVRRITISLL (SEQ ID NO: 185)

35 ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG  
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC  
AATGCAATCATCATTCCACCATTGTCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT  
CCTTGCCATCCTCTCTTGCTCTGAGATTTGCTACACCTTCATCATTGTACCCAAGATGCTGG  
40 TTGACCTGCTGTCCCAGAAGAAGACCATTTCTTTCCTGGGCTGTGCCATCCAAATGTTTTCC  
TTCCTCTTCCTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT  
AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA  
GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTCA  
CCTGCCTTTTTATTCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGTCTCA  
45 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC  
CTGGCTATCCCCTTATTGTTGATCTTGGTGCCTATGTTACATCCTCTCTGCCATACTTCA  
GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTCTACCTGTGTATCTCACCTCATTATTG  
TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAACCTACTCCTCA  
AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA  
50 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAT  
TTCCCTGTTGTAA (SEQ ID NO: 186)

**AOLFR101 sequences:**

MDTGNWSQVAEFILGFPHLQGVQIYLFLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI  
55 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL  
HYPTLMTPTLCAELAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDPFPVLSLACTDTSINV



LVDFVINSCKILATFLLILCSYVQHICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK  
KSYSLDYDQALAVVYSVLTPFLNPFYSLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCCATCTCC  
5 AGGGTGTCCAGATTTATCTCTTCTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA  
AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT  
TTGTGAGCATTCTCTCCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG  
GCAAACTTGCTCAGTGAGAAAAAGACCATTTCATTCTCTGGGTGTCTCCTGCAGATCTATT  
10 TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA  
TTTAGCCATCTGCCGGCCCCCTCCACTACCCAACCCCTCATGACCCCAACACTTTGTGCAGAG  
ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTGATTT  
CACGCCTCCCATTTCTGTGGCCCCAATCGCATTACGACAGCTCTTTGTGACTTCCCTCCTGTG  
CTGAGTTTGGCTTGCACTGATACGTCTATAAATGTCCTAGTAGATTTTGTATAAATTCCTG  
15 CAAGATCCTAGCCACCTTCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC  
TCAGAATTCCTCAGCTGCCGGCAAGAGGAAGGCCATCTCCACGTGTGCCTCCCACTTCAC  
TGTGGTTCTCATCTTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTAC  
TCACTGGACTATGACCAGGCCCTGGCAGTGGTCTACTCAGTGCTCACACCTTCTCAACC  
CCTTCATCTACAGCTTGCACAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA  
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

20

**AOLFR102 sequences:**

MPVGKLVFNQSEPTFVFRAFTTATEFQVLLFLLFLLYLMILCGNTAIWVVCVTHSLRTPMYF  
FLSNLSFLELCYTTVVVPLMLSNILGAQKPISLAGCGAQMFFVTLGSTDCFLAIMAYDRYVAI  
CHPLHYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLPFCGHHQEINHFLCDVPPVLRRLACA  
25 DIRVHQAVLYVVSILVLTIPFLICVSYVFITCAILSIRSAEGRRRAPSTCSFHLTVVLLQYGCCSL  
VYLRPRSSTSEDEDSQIALVYTFVTPLNPLLYSLRNKDKGALRSAIRKAASDAN (SEQ ID  
NO: 189)

ATGCCTGTGGGGAACTTGTCTTCAACCAGTCTGAGCCCACTGAGTTTGTGTTCCGTGCGT  
30 TCACCACAGCCACTGAATTCAGGTTCTTCTCTTCTTCTTCTCCTCCTCTACTTGATG  
ATCCTCTGTGGCAACACAGCCATCATCTGGGTGGTGTGCACACACAGCACCCCTCCGCACCC  
CGATGTATTTCTTCTGTCCAACCTGTCTTCTTCTGGAACCTCTGCTACACCACCGTGGTAGTA  
CCCTTGATGCTTTCCAACATTTTGGGGGGCCAGAAGCCCATTTTGGTTGGCTGGATGTGGGG  
35 CCCAAATGTTCTTCTTTGTACCCCTCGGCAGCACGACTGTTTCTTCTTGGCGATCATGGCC  
TATGACCGCTATGTGGCTATCTGCCACCCGCTGCACTACACCCTCATCATGACCCGCGAGC  
TGTGCACGCAGATGCTGGGTGGGGCCCTGGGCCTGGCCCTCTTCCCCTCCCTGCAGCTCAC  
CGCCTTAATCTTACCCCTGCCCTTTTGGCGCCACCAGCAAGAAATCAACCACTTCCTCTGCG  
ATGTGCCTCCCGTCTGCGCCTGGCCTGCGCTGACATCCGCGTGCACCAAGGCTGTCTCTA  
TGTCGTGAGCATCCTCGTGCTGACCATCCCTTCTGCTCATCTGCGTCTCTACGTGTTCA  
40 TCACCTGTGCCATCCTGAGCATCCGTTCTGCCGAGGGCCGCCCGGGCCTTCTCCACCTG  
CTCCTTCCACCTCACCGTGGTCTGCTGCACTATGGCTGCTGCAGCCTCGTGTACCTGCGTC  
CTCGGTCCAGCACCTCAGAGGATGAGGACAGCCAAATCGCGTTGGTCTACACCTTTGTAC  
CCCCTTACTCAACCTTTGCTTTACAGCCTTAGGAACAAGGATGTCAAAGGTGCTCTGAGG  
AGTGCCATTATCCGTAAAGCAGCCTCTGACGCCAACTGA (SEQ ID NO: 190)

45

**AOLFR103 sequences:**

MAEMNLTLVTEFLLIAFTEYPEWALPLFLLLLFMYLITVLGNLEMIILIMDHQLHAPMYFLLSH  
LAFMDVCYSSITVPQMLAVLLEHGAALS YTRCAAQFFLFTFFGSIDCYLLALMAYDRYLAVCQ  
PLLYVTILTQQARLSLVAGAYVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLKLTCGESYT  
50 QEVLIIMFAIFVIPASMVVILVSYLFIIVAIMGIPAGSQAKTSTCTSHLTA VSLFFGTLIFMYLRG  
NSDQSSEKNRVSVLYTEVIPMLNPLYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)

ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCTCCTTATTGCATTCACTGAATATC  
CTGAATGGGCACTCCCTCTCTTCTTCTTGTATTATTTATGTATCTCATCACCGTATTGGGG  
55 AACTTAGAGATGATTATTCTGATCCTCATGGATCACCAGCTCCACGCTCCAATGTATTTCT  
TCTGAGTCACCTCGCTTTCATGGACGTCTGCTACTCATCTATCACTGTCCCCAGATGCTGG



CAGTGCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCTTTCT  
 GTTCACCTTCTTTGGTTCCATCGACTGCTACCTCTTGGCCCTCATGGCCTATGACCGCTACT  
 TGGCTGTGTGCCAGCCCTGCTTTATGTCACCATCCTGACACAGCAGGCCCGCTTGAGTCT  
 TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCCTTGGTGCGGACAGTCTCAGCCTTC  
 5 ACTCTCTCCTTCTGTGGAACCAGTGAGATTGACTTTATTTTCTGTGACCTCCCTCCTCTGTT  
 AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAGTGCTGATTATTATGTTTGCCATTTTT  
 GTCATCCCTGCTTCCATGGTGGTGATCTTGGTGTCTACCTGTTTATCATCGTGGCCATCAT  
 GGGGATCCCTGCTGGAAGCCAGGCCAAGACCTTCTCCACCTGCACCTCCACCTCACTGCT  
 GTGTCACTCTTCTTTGGTACCCTCATCTTCATGTACTTGAGAGGTAACCTCAGATCAGTCTTC  
 10 GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGGTCATCCCCATGTTGAATCCCCTC  
 ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC  
 AAGTTGTCCTAA (SEQ ID NO: 192)

#### AOLFR105 sequences:

15 MQGLNHTSVSEFILVGFSAPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC  
 ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFSSFSFGFTHSFLLTVMGYDRYVAICHPL  
 RYNVLM SLRGCTCRVGCSWAGGLVMGMVVTSAIFHLAFCGHKEIHFFCHVPPLKLACGDD  
 VLVVAKGVGLVCITALLGCFLLILLSYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS  
 VIYLPKGPQSPGDTLMGITYTVLTPFLSPIIFSLRNKELKVAMKKTCTFKLFPQNC (SEQ ID  
 20 NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC  
 CCACCTCCAGCTGATGCTCTTCTCTGCTGTTCTGCTGATGTACCTGTTACGCTGCTGGGCA  
 ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT  
 25 CCTGTGTGCCCTCTCCATCACCAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTG  
 GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTCTGGCCTGTGCCAGTCAGATGTTCTT  
 CTCCTTCAGCTTCGGCTTCACCCACTCCTTCTCTGCTCACTGTGATGGGCTACGACCGCTACG  
 TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG  
 GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTTC  
 30 CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTCTTCTGCCACGTGCCACCTCTGTT  
 GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGAT  
 CACGGCCCTGCTGGGCTGTTTTCTCCTCATCCTCCTCTCCTATGCCTTCATCGTGGCCGCCA  
 TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT  
 CACTGTGGTGGTGTGCTGACTATGGCTTTGCCTCCGTCATTTACCTGAAGCCCAAAGGTCCC  
 35 CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCCTCACACCCTTCTCA  
 GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT  
 CACCAAACCTCTTCCACAGAACTGCTGA (SEQ ID NO: 194)

#### AOLFR106 sequences:

40 METANYTKVTEFVLTLGLSQTPEVQLVLFVIFLSFYLFILPGNIICTISLDPHLTSPMYFLLANLA  
 FLDIWYSSITAPEMLIDFFVERKHSFDGCIQLFFLHFAGASEMFLLTVMAFDLYTAICRPLHYA  
 TIMNQRLCCILVALSWRGGFIHSHQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM  
 ICSSGLISVCLIALLLMSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVVLMFGPSIYIYARPF  
 SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

45 ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC  
 CAGAGGTCCAACTAGTCCTATTGTTATATTTCTATCCTTCTATTTGTTATCCTACCAGGA  
 AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCT  
 GTTGGCTAATCTGGCCTTCTTGATATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA  
 50 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT  
 CTTACACTTTGCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA  
 CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG  
 GTGGCTCTCTCCTGGAGGGGGGGCTTCATTATTCTATCATACAGGTGGCTCTCATTGTTCT  
 GACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACAGGTTGT  
 55 CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG  
 ATCTCTGTGGTGTGTTGATTGCTCTGTTAATGTCTATGCCTTCTTCTGGCCTTGTTCAA

GAAACTTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT  
 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCGTT  
 TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATCCCTTTACGTAATCCCATT  
 TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAATATA  
 5 TTTTGTGTAAAGAGAAGTGA (SEQ ID NO: 196)

**AOLFR107 sequences:**

MELWNFTLGSFILVILNDSGSPHELLCATITILYLLALISNGLLLAITMEARLHMPMYLLLGQ  
 LSLMDLLFTSVVTPKALADFLRRENTISFGGICALQMFLALTMGGAEDLLAFMAYDRYVAICH  
 10 PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYHPCRAQEIRHLLCEIPHLKLVACAD  
 TSRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGA  
 ATFMVLPSSFHSTRQDNIIISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMPLPAHSTL  
 (SEQ ID NO: 197)

15 ATGGAGCTCTGGAACCTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA  
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG  
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGGCTCCACATGCCCATGTACCTC  
 CTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTACATCTGTTGTCACTCCCAAGGCCCT  
 TGCGGACTTTCTGCGCAGAGAAAACACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT  
 20 CTGGCACTGACAATGGGTGGTGTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT  
 ATGTGGCCATTTGTCATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT  
 CATGGTGGCCACGTCTGGATCCTGGCATCCCTAAGTGGCCTAATATATACCGTGTATACC  
 ATGCACTATCCCTTCTGCAGGGCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCACT  
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT  
 25 GACCTTCCTGATTCCCTCTCTTGCTGCTATACTGGCCTCCTATACACAAATTCTACTCATG  
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACCTGCTCTTCCACCT  
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCAGGTTCTTCC  
 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAA  
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCTGGG  
 30 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

**AOLFR108 sequences:**

MCSFFLCQTKQAKISMGEENQTFVSKFIFLGLSQDLQTQILLFILFLIYLLTVLGNQLIILIFLD  
 SRLHTPMYFFLRNLSFADLCFSTSIQVQLVHFLVKRKTISFYGCMQTQIIVFLLVGCTECALLAV  
 35 MSYDRYVAVCKPLYYSTIMTQRVCLWLSFRSWASGALVSLVDTSTFPHLPYWGQNIINHYFCE  
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIIISTVIQMQSGEGRKAFSTCGSHLI  
 VVVLFGSGIFTYMRPNSTTKELDKMISVFYTA VTPMLNPIIYSLRNKDVKGALRKL VGRKC  
 FSHRQ (SEQ ID NO: 199)

40 ATGTGTTCTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA  
 ACCAAACCTTTGTGTCCAAGTTTATCTTCCTGGGTCTTTCACAGGACTTGCAGACCCAGAT  
 CCTGCTATTTATCCTTTTCTCATCTTTATCTGCTGACCGTGCTTGGAACCCAGCTCATCA  
 TCATTCTCATCTTCTGGATTCTCGCCTTCACACTCCCATGTATTTTTTTCTTAGAAATCTCT  
 CCTTGCAGATCTCTGTTTCTCTACTAGCATTTGCCCTCAAGTGTTGGTTCACTTCTTGGTA  
 45 AAGAGGAAAACCATTTCTTTTATGGGTGTATGACACAGATAATTGTCTTTCTTCTGGTTG  
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTCTGCAA  
 GGGCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCAAGTCTCT  
 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATACCAGCTTTACTTTCCATCTTCCCTACTG  
 GGGACAGAAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC  
 50 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCCTCCTGGCCC  
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT  
 GGGGAAGGGGAGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCTCTCT  
 CTATGGGTGAGGAATATTCACCTACATGCGACCAAACTCCAAGACTACAAAAGAACTGGA  
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC  
 55 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAACTAGTTGGGAGAAAGTGCTTCTCT  
 CATAGGCAGTGA (SEQ ID NO: 200)

**AOLFR109 sequences:**

- MLRNGSIVTEFILVGFQSSSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG  
 HLSLLDVCFITTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGVAEICILLAFMAYDRYVAICY  
 5 PLNYVPIISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL  
 WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN  
 PHSTHGPDKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:  
 201)
- 10 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTTACGACAGAGCTCCA  
 CTCCACACGAGCATTGCTCTTTGCCCTCTTCTGGCCCTCTACAGCCTCACCATGGCCATG  
 AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTA  
 TCTTCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCCTACCATCCACAGATG  
 TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT  
 15 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCTATGACCGT  
 TATGTTGCTATCTGCTACCCACTTAACATATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA  
 GGCTTGTGGGAACTGCCTGGTTCTTTGGGCTGATCAATGGCATCTTCTCGAGTATATTTT  
 ATTCCGAGAGCCCTTCCGCAGAGACAACCACATAGAAAGCTTCTTCTGTGAGGCCCCCAT  
 GTGATTGGCCTCTCTTGTGGGGACCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA  
 20 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCCTATGTGCACATCCTGGCCACC  
 ATCCTCAGCAAAGCCTCCTCCTCAGGTCGGGGGAAGACTTTCTCTACTTGTGCTCTCACC  
 TGACTGTGGTCATCTTTCTCTACACTTCAGTATGTTCTCTTACATGAACCCCCACAGACA  
 CATGGGCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCATGTGCA  
 ACCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG  
 25 GAAGAACCAGGCTGGCCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

**AOLFR110 sequences:**

- MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL  
 DASYSFIVAPRMLVDFLSEKKVISYRGCTQLFFLHFLGGGEGLLLVMMAFDRIYIAICRPLHCST  
 30 VMNPRACYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVRQVIKLACTDMFVVEL  
 LMVFNGLMTLLCFLGLLASVAVILCHVRRASEGKNKAMSTCTTRVIIIIMFGPAIFIYMCPP  
 RALPADKMVSLFHTVIFPLMNPIMYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:  
 203)
- 35 ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC  
 AAGATATTAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA  
 AATTTTCTCATTATTTTACCATAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT  
 TCTGGGCAACTTGGCCTTCCTGGATGCATCCTACTCCTTCATTGTGGCTCCCAGGATGTTGG  
 TGGACTTCCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT  
 40 CTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC  
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA  
 TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCTC  
 CGCTTGCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTGTGATGTCCGACAGGTCA  
 TCAAGCTGGCTTGACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT  
 45 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCCTATGCAGTCATCCTCTGCCATGTT  
 GTAGGGCAGCTTCTGAAGGGAAGAAACAAGGCCATGTCCACGTGCACCACTCGTGTCTTA  
 TTATACTTCTTATGTTTGGACCTGCTATCTTCACTACATGTGCCCTTTAGGGCCTTACCA  
 GCTGACAAGATGGTTTCTCTTTTACACAGTGATCTTTCCATTGATGAATCCTATGATTTA  
 TACCCTTCGCAACCAGGAAGTGAAACTTCCATGAAGAGGTTATTGAGTCGACATGTAGTC  
 50 TGTCAAGTGGATTTATAATAAGAACTGA (SEQ ID NO: 204)

**AOLFR111 sequences:**

- MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCILHSILFLLIYLCALM  
 GNVLIIMITTLDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSIHNNSISFLGCVSQVFLLLSS  
 55 ASAELLLLTVMSFDRIYAICHPLHYDVIMDRSTCVQRATVSWLYGGIAVMHTAGTFSLSYCG  
 SNMVHQFFCDIPQLLAISCSENLIREIALILINVLDFFCCFVVIITYVHVSTVKIPSTEGQSKAY

SICLPHLLVVLFLSTGFIAYLKPASESPSILDAVISVFYTMLPPTFNPIIYSLRNKAIKVALGMLIKG  
KLTKK (SEQ ID NO: 205)

5 ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT  
TTTCCTGCAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA  
TGGGGTTTTCTACCAATAAAAATATGTGCATTTTGCATTTCGATTCTCTTCTTGTTGATTTAT  
TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACCTTTGGACCATCATCTCC  
ACACCCCGTGTATTTCTTCTTGAAGAATCTATCTTTCTTGGATCTCTGCCTTATTTTCAGTC  
ACGGCTCCCAAATCTATCGCCAATTCTTTGATACACAACAACCTCCATTTTCATTCTTGGCTG  
10 TGTTCCTTCCAGGTCTTTTGTGCTTTCTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA  
TGTCTTTTGACCGCTATACTGCTATATGTCACCTCTGCACTATGATGTCATCATGGACAGG  
AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGTCTGATTGCTGTGATGC  
ACACAGCTGGCACCTTCTCCTTATCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT  
GACATTCCCCAGTTATTAGCTATTTCTTGTCTCAGAAAATTTAATAAGAGAAATTGCACTCA  
15 TCCTTATTAATGTAGTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC  
GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT  
GCCITCCACACTTGCTGGTTGTGTTATTTCTTCCACTGGATTCAATTGCTTATCTGAAGCCA  
GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC  
AACCTTTAATCCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG  
20 TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

**AOLFR113 sequences:**

MKFVWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP  
SVVTCSSSQSSDWMQLCTHLCTTLVFFPSWSCGIQLPLSLRCCLIFSVRRKPFLQDASFRPTSS  
25 TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF  
CAYNEIQHIFCDFPPLLSLACKDTSANILVDFAINAFILITFFIMISYARIUGAVLKIKTASGRKK  
AFSTCASHLAVVLFFGSIIFMYVRLKKSYSYSLTLDRTLAVVSVLTPMVNPIIYSLRNKEIKAIKR  
TIFQKGDKASLAHL (SEQ ID NO: 207)

30 ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA  
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC  
CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA  
GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA  
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA  
35 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG  
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG  
CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA  
GAATTCTCACGCCTCAAGTGATGCTGGAATGAGTATGGCCATCACCATCAGAGCTATCAT  
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT  
40 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA  
GCAGTCTCTACAGTCTGATTGGTTCCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT  
GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA  
AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG  
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCAAGTCCTGC  
45 TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC  
CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC  
CTGGGTTTCATGA (SEQ ID NO: 208)

**AOLFR114 sequences:**

50 MERINHTSSVSEFILLGLSSRPEDQKTLFVFLIVYLVTITGNLLIILAIRFNPHLQTPMYFFLSFLS  
LTDICFTTSVVPKMLMFLSEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDRYVAVCDPF  
HYVTTMSHHHCVLLVAFSCSFPHLHSLHTLLNRLTFCDNSVIHHFLCDLSPVLKLCSSSIFVN  
EIVQMTEAPIVLVTRFLCIAFSYIRILTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQP  
PSTYAVKDHVATIVYTVLSSMLNPFYISLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

55

ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC  
 GGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCCTCATCGTGTACCTGGTCACCATAAC  
 AGGGAACCTGCTCATCATCCTGGCCATTGCTTCAACCCCATCTTCAGACCCCTATGTATT  
 TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCAAGATG  
 5 CTGATGAACCTCCTGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT  
 ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG  
 CTATGTGGCGTCTGTGACCCTTTCCACTATGTCAACCACCATGAGCCACCACCCTGTGTCC  
 TGCTGGTGGCCTTCTCCTGCTCATTTCTCACCTCCACTCACTCCTGCACACACTTCTGCTG  
 AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCCTTTCTCTGTGACCTCAGCCCTGT  
 10 GCTGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT  
 ATTGTTTTGGTGACTCGTTTTCTCTGCATTGCTTTCTCTTATATACGAATCCTCACTACAGT  
 TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA  
 CCGTGGTGACGCTCTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC  
 GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTGTGCATCCATGCTCAATCCTT  
 15 TTATCTACAGCCTGAGAAACAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA  
 GATCCTAG (SEQ ID NO: 210)

# **AOLFR115 sequences:**

MEGFYLRSHLQGMGKPGRVNQTTVSDFLLLGLSEWPPEQLLFGIFLGMVLTVMVGNLLII  
 20 LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD  
 NCLLAVMAYDRYVAICQPLHYSTMSQPQLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK  
 AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPLLLIVFSYVRIFWAVFVISSPGGRWKA  
 FSTCGSHLTVVLLFYGLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLRNRDMKEALG  
 KLFVSGKTFFL (SEQ ID NO: 211)

25 ATGGAAGGTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA  
 GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC  
 AGCCTCTTCTGTTTGGCATCTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC  
 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA  
 30 CCTGTCAATTAAGTATGCCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAACATTC  
 ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGCACAGCTATATTCTCCTTATG  
 TTTGCTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT  
 GCCAACCACTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCTAATGCTGGGTGT  
 GTGCTGGGTGCTAACCACTGTCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT  
 35 TTCTGTGCCCAGAAAGCCATCCCTCATTTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC  
 CTGCTCAGATAACCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCTCCTACT  
 GTTCCCTCTCTGCTGATCGTCTTCTCCTATGTCCGCATTTTCTGGGCTGTGTTTGTCTCTC  
 ATCTCCTGGAGGGAGATGGAAGGCCTTCTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG  
 CTCTTCTATGGGTCTCTTATGGGTGTGATTTACTTCTCCATCAACTACTCTACAGAGAG  
 40 GGAAAGTAGGGCTGCTGTTCTATATGGTGATTATCCACGCTAAACCATTCATTTAT  
 AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAACTTTTTGTGCTGGAACAAACA  
 TTCTTTTTATGA (SEQ ID NO: 212)

# **AOLFR116 sequences:**

45 MDEANHSVVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN  
 LSIINLVFCSSTAPKMIYDLFRKHTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH  
 YLTIMNPQRCLFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV  
 TANSGFISLASFLILISYIFLVTQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPPTSHLD  
 KFLAIFDAVITPVLNPVITYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

50 ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTGAGTCTCTGACTCGC  
 GGAAGATCCAGCTCCTCCTCTCTCTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA  
 AATCTCCTCATTTGTGCTAACTGTGACCTCTGACCTCGTTTACAGTCCCCCATGTACTTCT  
 GCTGGCCAACCTTTCCATCATCAATTTGGTATTTTGTCTCCACAGCTCCCAAGATGATTT  
 55 ATGACCTTTTACAGGAAGCACAAGACCATCTCTTTTGGGGGCTGTGTAGTTTACAGATCTTCTT  
 TATCCATGCAGTTGGGGGAACTGAGATGGTGCTGCTCATAGCCATGGCTTTTGACCGATAT

GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT  
 TTTTAGTCATTTCTGGATTATAGGTATTATTCACTCAGTGATTGAGITGGCTTTTGTGTA  
 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTGTGATCTTCCTCGATTAT  
 CAAACTGGCTTGCATAGAGACCTACACATTGGGATTCATGGTTACTGCCAATAGTGGATTT  
 5 ATTTCTCTGGCTTCTTTTTTAATTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTTCAG  
 AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTCAGCTCATGTCATTGTGG  
 TGGTTTTGGTCTTTGGGCCATTAATCTTTTTCTATATTTTCCATTTCCACATCACATCTTG  
 ATAAATTCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTTGAATCCAGTCATCTATACT  
 10 TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC  
 AGTAAAATCTTTTAA (SEQ ID NO: 214)

#### AOLFR117 sequences:

MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLLAMTLGNSTEVTEFYLLGFGA  
 QHEFWCILFIVFLLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT  
 15 EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPPYVAICKPLHYTVMSRVCIRLVAGSYI  
 MGSINASVQTGFTCSLSFCKSNSINHFFCDVPPILALSCSNVDNIMLLVVFVGSNLIFTGLVVIFS  
 YIYIMATILKMSSSAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQSHSNNSQENMKVAFIFYGTVI  
 PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215)

20 ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA  
 GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTCTGGGTCCTTCTCTGGTC  
 ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC  
 TTCTGGGATTTGGTGCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCCTTCTCATC  
 TATGTGACCTCCATAATGGGTAATAGTGGAATAATCTTACTCATCAACAGATTCCAGAT  
 25 TTCAAACACTCACGTACTTTTTTCTACAACATTTGGCTTTTGTGATATCTGTTACACTCT  
 GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTTCAGG  
 GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAAGTGAAGTGTATCTCCTGGCT  
 ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCCTTCACTATACTGTAATCATGT  
 CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC  
 30 TGTACAAACAGGTTTTACATGTTCACTGTCCTTCTGCAAGTCCAATAGCATCAATCACTTTT  
 TCTGTGATGTTCCCCCTATTCTTGCTCTTTCATGCTCCAATGTTGACATCAACATCATGCTA  
 CTTGTTGTCTTTGTGGGATCTAACTTGATATTCAGTGGGTTGGTCGTCATCTTTTCTACAT  
 CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA  
 ACATGTGCTTCCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT  
 35 GCAGTCTCATTCTAATAATCCCAGGAAAATATGAAAGTGGCCTTTATATTTTATGGCACA  
 GTTATTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT  
 TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

#### AOLFR118 sequences:

40 MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWLSLPLALLYLSALAANTLILIIHWQNPSLQQ  
 PMYIFLGILCMVDMGLATTIIPKILAFWFDKVISLPECFAQIYAIHFFVGMESGILLCMAFDY  
 VAICHPLRYPISIVTSSLILKATLFMVLRLNGLFVTPVPLAAQRDYCSKNEIEHCLCSNLGVTSLA  
 CDDRRPNSICQLVLAWLGMGSDLSLILSYILILYSVLRNLNSAEAAAKALSTCSSHLTLILFFYTIV  
 VVISVTHLTEMKATLIPVLLNVLHNIIPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID  
 45 NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCCAGGTCTCTGAGTT  
 CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCCTGGCA  
 CTA CTGTATCTCTCAGCACTTGCTGCAACACCCTCATCCTCATCATCTGGCAGAACCC  
 50 TTCTTTACAGCAGCCCATGTATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG  
 CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGATGCCAAGGTTATTAGCCTC  
 CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT  
 ACTCTGCATGGCTTTTGATAGATATGTGGCTATTTGTCAACCCTCTTCGCTATCCATCAATTG  
 TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTTCATGGTGCTGAGAAATGGCTTATTTGTC  
 55 ACTCCAGTGCCTGTGCTTGACAGCACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT  
 GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT

TTGCCAGTTGGTTCTGGCATGGCTTGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA  
TATATTTTGATTCTGTACTCTGTACTTAGACTGAACTCAGCTGAAGCTGCAGCCAAGGCC  
TGAGCACTTGTAGTTCACATCTCACCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT  
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC  
5 ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAACTTAG  
GGCAGCCTTCCAAAAGGTGCTGTTTGGCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:  
218)

**AOLFR119 sequences:**

10 MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP  
MYFFFGHALSLIDLLTCTTLPNALCIFWFSLKEINFNACLAQMFFVHGFTGVESGVLMLMALD  
RYIAICYPLRYATTLNPIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL  
SCASIKVNVIIYGLMVALLIGVFDICCSLSYTLILKAAISLSSSDARQKAFSTCTAHISAIHITYVPA  
15 FFFFAHRFGGHTIPPSLHIVANLYLLLPTLNPVIVGVKTKQIRKSVIKFFQGDKGAG (SEQ ID  
NO: 219)

ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT  
TCTTAATGGAATACCTGGTCTGGAAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA  
ATGTACATCATCTTCCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC  
20 CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG  
CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA  
ATGCTTGCTTGGCCCAGATGTTCTTTGTTTCATGGGTTCACAGGTGTGGAGTCTGGGGTGCT  
CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCCTTTCGCTTATGCTACCACAC  
TCACCAACCCTATCATTGCCAAGGCTGAGCTTGGCACCTTCCTGAGGGGTGTATTGCTGAT  
25 GATTCCCTTCCCATTCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCCAT  
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT  
CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTGTTGACATTTGTTGTATATCTTTGTCTT  
ACACTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT  
CAGCACCTGCACTGCCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT  
30 TCTTTGCCACCGTTTTGGGGGACACACAATTCCCCCTTCTCTTCACATCATTGTGGCTAAT  
CTTTATCTTCTTCTTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT  
ACGCAAGAGTGTGCATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

**AOLFR120 sequences:**

35 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFTMYLFTLVENLAAILVVGLDHLRLRRPMYF  
FLTHLSLEIWIYTSVTPKMLAGFIGVDGGKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY  
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPIPLPIYLLSQLTCGPNVIDHFSCDASPLALS  
CSDVTWKETVDFLVSLAVLLASSMVIASVGNIVWTLHIRSAAERWKAFSTCAAHLTVVSLF  
40 YGTLFFMYVQTKVTSSINFNKVVSFYSVTPMLNPLIYSLRNKEVKGALGRVFSLNFWKQG  
(SEQ ID NO: 221)

ATGCAACCATATACCAAAAACCTGGACCCAGGTAACCTGAATTTGTCATGATGGGCTTTGCTG  
GCATCCATGAAGCACACCTCCTCTTCTTCATACTCTTCCTCACCATGTACCTGTTACCTTG  
GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT  
45 ATTTCTTCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG  
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT  
CCCAGCTCTTCATCTTACCTTTCTTGGGGCAACTGAGTGTTTCTACTGGCTGCCATGGCC  
TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCCTGGGGCAC  
CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCTCACACCCATCTTGCCAATCT  
50 ACCTCTTGTCTCAGCTAACATTTTGTGGCCCAATGTCATTGACCATTCTCCTGTGATGCC  
TCACCTTGCTAGCCTTGTCTGTCTCAGATGTCACTTGAAGGAGACTGTGGATTCTCTGG  
TGTCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCATTGCTGTGTCCTATGGCAACATCGTC  
TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG  
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG  
55 GTGACCTCCTCCATCAACTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCAT



GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTCGAGTC  
TTTTCTCTCAACTTTTGGGAAGGGACAGTGA (SEQ ID NO: 222)

**AOLFR121 sequences:**

5 MKRKNFTEVSEFIFLGFSSFGKHQITLFVVFLTVYILTLVANIIVTIIICIDHHLHTPMYFFLSMLA  
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFVILATNNCFLLTAMGYDRYVAICRPLRY  
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLPFCGTVDHFFCDIYPVMKLSCIDTTINEII  
NYGVSSFVIFVPIGLIFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPKSES  
SIEKDLVLSVTTYTIITPLLNPVVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

10 ATGAAGAGAAAGAACTTCACAGAAGTGTGAGAATTCATTTTCTTGGGATTTTCTAGCTTTG  
GAAAGCATCAGATAACCCCTCTTTGTGGTTTTCCTAACTGTCTACATTTTAACTCTGGTTGCT  
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTTCTT  
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT  
15 TTGAGCCTCATTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT  
TTTTGTTATCTTGGCCACTAATAATTGCTTCTGCTTACTGCAATGGGGTATGACCGCTATG  
TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCAGCT  
GGTGTGTGGGTCCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT  
AATTTGCCGTTCTGTGGCACAGTGGTAGACCACTTCTTTTGTGACATTTACCCAGTCATGA  
20 AACTTTCTTGCATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAGTTCATTTGT  
GATTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTCTCTTCCATCCTTC  
AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT  
GGTTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAAGTTCA  
ATAGAAAAAGACCTTGTTCTCTCAGTGACGTACACCATCATCACTCCCTTGCTGAACCTG  
25 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA  
ATATTTCTTAA (SEQ ID NO: 224)

**AOLFR122 sequences:**

30 MEWENQTLVEFFLKGHSVHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL  
SFLDICYTTSIPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMMAFDYVAICNPLR  
YPIIMSKNAYVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCIELAVMKLACADISGN  
EFLMLVATILFTLMPLLLIVISYSLIISILKHSSEGRSKAFSTCSAHLTVVIIIFYGTILFMYMKPKS  
KETLNSDDL DATDKIISM FYGVMT PMMNPLIYSLRNKD VKEA VKHLNRRFFSK (SEQ ID NO:  
225)

35 ATGGAATGGGAAAACCAAACCATTTCTGGTGGAATTTTTTCTGAAGGGACATTCTGTTCAAC  
CAAGGCTTGAGTTACTCTTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG  
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT  
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG  
40 TGAGCTTCTTTTCAAGAAAGAAAGACCATTTCTTTTCTGGCTGTGCAGTGCAGATGTTCTT  
GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG  
TGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT  
GGCTGTTGGGTCCTGGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA  
CAATTGCCTTTCTGCAGGAAGAATGTCATCAATCATTTCTCATGTGAAATTCTAGCTGTCAT  
45 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCCTCATGCTTGTGGCCACAATATTG  
TTCACATTGATGCCACTGCTCTTGATAGTTATCTCTTACTCATTAATCATTTCCAGCATCCT  
CAAGATTCACTCCTCTGAGGGGAGAAGCAAAGCTTTCTCTACCTGCTCAGCCCATCTGACT  
GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA  
CACTTAATTCAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT  
50 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT  
AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

**AOLFR123 sequences:**

55 MYRFTDFDVSNISIYLNHVLFYTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL  
IMYMIILLGNSLLIHTILDSRLHTPMYFFLGNSFLDICYTSSSIPMLIIFMSERKSISFIGCALQM  
VVSGLGSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLQLTVLT



MMLPFCGNNVIDHITCEILALLKLVCSDITINVLMITVTNIVSLVILLLLIFISYVFILSSILRINCAE  
GRKKAFSTCSAHSIVVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV  
KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

5 ATGTACAGATTIACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCTTTT  
CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT  
GACTGAATTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCTGC  
TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC  
TTGGATTCTCGCTCCATACTCCCATGTATTTCTTTCTTGAAACCTCTCATTCTTGACAT  
10 CTGTTACACATCCTCATCCATTCTCCAATGCTTATTATATTATGTCTGAGAGAAAAATCCA  
TCTCCTTCATTGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT  
GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGTACT  
CCATCATCATGAACGGAGTGCTGTATGTGCAAATGGCTGCATGGTCTGGATCATAGGCTG  
TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC  
15 ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAACTTGTTTGTTCAGATATCACCAT  
CAATGTGCTTATCATGACAGTGACAAATATGTTTCACTGGTGATTCTTCTACTGTAAATTT  
TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAA  
AAAGCCTTCTCTACCTGTTTCTGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT  
TTTTATGTACATGAAACCCAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGGCTG  
20 TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG  
TCAAAGAGGCTGTAAAGAAAGTCCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ  
ID NO: 228)

**AOLFR124 sequences:**

25 MNHSVVTEFIILGLTKKPELQGIIFLFLIVYLVAFLGNMLIIIAKIYNNTLHTPMYVFLLTLAVV  
DIICTSIIPKMLGTMLTSENTISYAGCMSQLFLTWSLGAEMVLFTTMAYDRYVAICFPLHYST  
VMNHHMCMVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPLLALSCSPVRINEV  
MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVGKRAKAFSTCSSHLTVVTLYSPVIYTYIRPASS  
YTFERDKVVAALYTLVPTLNPVMVYSFQNRMQAGIRKVFAFLKH (SEQ ID NO: 229)

30 ATGAATCACAGCGTTGTAACCTGAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC  
AGGGAATTATCTTCCTCTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC  
ATCATCATTGCCAAAATCTATAACAACACCTTGCATACGCCCATGTATGTTTCTTCTGAC  
ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT  
35 GCTAACATCAGAAAATACCATTTTCATATGCAGGCTGCATGTCCCAGCTCTTCTTGTTCACA  
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA  
TTTGTTTCCCTCTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC  
ATGGTCATGGCTATTGCAGTCACCAATTCTGGGTGCACACAGCTCTTATCATGAGGTTGA  
CTTTCTGTGGGCCAAACACCATGACCACTTCTTCTGTGAGATAACCCCATGCTGGCTTTG  
40 TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCTGGCCA  
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTGCTATTCTCCGTATC  
CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG  
ACCTTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA  
AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCACATTAAACCCGATGGTG  
45 TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA  
CACTAG (SEQ ID NO: 230)

**AOLFR125 sequences:**

50 MTNQQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAMYFFLRH  
LSFLDLCLISATVPKSILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSYDRYAAICCPHLC  
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSEKHA  
ISVSVAIGVCYAFSCLVCIVVSYYVIFSAVLRISQRQROSKAFSNCVPHLIVTVFLVTGAVAYL  
KPGSDAPSILDLLVSFYSVAPPTLNPVTYCLKNKDIKSALSKVLWNVRSSGVMKDD (SEQ ID  
NO: 231)

55

ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC  
 TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTA  
 GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCG  
 ACATTTGTCCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCCAAATCCATCCTCAACT  
 5 CTGTGCGCTCCACTGACTCCATCTCCTTCCCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA  
 CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA  
 TCTGCTGCCCCCTACACTGTGAGGCTGTCATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC  
 TCTGTCTGGCTCAACAGAGGGGCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCTG  
 AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT  
 10 CACTTGTTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA  
 TTTTCATGTTTAGTTTGCATTGTAGTTTCCTATGTGTACATTTTCTCTGCTGTGTTAAGGAT  
 ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAACTGTGTGCCTCACCTCATTGTTGTC  
 ACTGTGTTTCTTGTAAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT  
 TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT  
 15 ACTGTCTGAAGAACAGGACATTAAATCCGCTCTGAGTAAAGTCTGTGGAATGTTAGAA  
 CGAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

#### AOLFR126 sequences:

MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDCKIPLFLAFLVIYELITMGNLGLIVLIW  
 20 KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL  
 ATMAYDRYVAICKALLYPVMITNELCIQLLVLSFIGLLHALIHEAFSRLTFCNSNIIHFYCDII  
 PLLKISCTDSSINFLMVIFAGSVQVFTIGTILISYTIILFTILEKKSIRKAVSTCGAHLISVSLY  
 YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID  
 NO: 233)

25 ATGTTCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA  
 ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTTACATCAACCTGACTGTAAAAT  
 ACCGCTCTTCTGGCATTCTTGGTAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA  
 TTGTTCTCATCTGGAAAGACCCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA  
 30 GCCTTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG  
 CTAAGAGTAAGATGATATCTCTCTGAAATGCATGGTACAATTTTTTCCCTTGTAAACCACT  
 GTAACCACAGAATGTTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTGCA  
 AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTCAGCTATTAGTCTTGCA  
 TTTATAGGTGGCCTTCTTCATGCTTAATCCATGAAGCTTTTTTATTTCAGATTAACCTTCTG  
 35 TAATTCCAACATAATAACAACACTTTTACTGTGACATTATCCCATGTTAAAGATTTCTGTGTA  
 CTGATTCTCTATTAACTTTCTAATGGTTTTTATTTTCGCAGGTTCTGTTCAAGTTTTACCA  
 TTGGAACATTTCTTATATCTTATACAATTATCCTCTTTACAATCTTAGAAAAGAAGTCTATC  
 AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT  
 ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT  
 40 GATGGAGTCTCTATTTTACACTGTCATAGTTCCTTTATTAAATCCCATGATCTACAGCCTGA  
 GAAACAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAAGCAATGTTTAG (SEQ ID  
 NO: 234)

#### AOLFR127 sequences:

45 MSNEDMEQDNTLLTEFVLTGLTYQPEWKMPFLVFLVIYELITVWNLGLIALIWNDPQLHIPM  
 YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY  
 VAICKPLLYPVMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHFYCDIIPFMISCTD  
 PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLISVSLYYGPLIF  
 MYLRPASQADDQDMIDSVFYTHIPLNPIIYSLRNKQVIDSFTKMVKRNV (SEQ ID NO: 235)

50 ATGTCGAATGAGGACATGGAACAGGATAATAACAACATTGCTGACAGAGTTTGTCTCACA  
 GGACTTACATATCAGCCAGAGTGGAAAATGCCCCTGTTCTTGGTGTCTTGGTGATCTATC  
 TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTTCA  
 ATCCCCATGTACTTTTTTCTTGGGAGTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT  
 55 AACTCCCCAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC  
 ATGATTCAATTTTTTCTTTGCATTTGGTGGAACTACAGAAATGTTTTCTTGGCAACAAT

GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTATATCCAGTGATTATGAACAAT  
TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCCTCCATGCCTTAATTCA  
TGAAGTCCITTATATTAGATTAAACCTTCTGCAATTCTAACATAATACATCATTTTTACTGTG  
ATATTATACCACTGTTTATGATTTCTGTACTGACCTTCTATTAAATTTTCTAATGGTTTTTA  
5 TTTTGTCTGGCTCAATTCAGGTATTCACCATTGTGACAGTTCTTAATTTCTTACACATTTGCT  
CTTTTCACAATCCTAAAAAGAAGTCTGTTAGAGGGCGTAAGGAAAGCCTTTTCCACCTGTG  
GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT  
GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTC  
CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAACAAGTAATAGATTTCATTACAAA  
10 AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

**AOLFR128 sequences:**

METQNLTVVTEFILLGLTQSQDAQLLVFLVLIFYLILPGNFLIIFTIKSDPGLTAPLYFFLGNLA  
LLDASYSFIVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMADFDRYIAICRPLHY  
15 STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL  
LMVSNSSLILLSLFLGLLASVAVILCRIRESSEKSKAISTCTTHIIIFLMFGPAIFYTCTPFQAFP  
ADKVVSFLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMFC (SEQ ID NO: 237)

ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC  
20 AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCTCCCTGGA  
AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT  
TCTGGGCAACTTGGCCTTACTGGATGCATCTACTCCTTCATTGTGGTTCCAGGATGTTG  
GTGGACTTCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT  
TCTTGCATTTTCTTGGAGCGGGAGAGATGTTCTCCTCGTTGTGATGGCCTTTGACCGCTAC  
25 ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT  
TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG  
CACTTGCCTTTCTGTGGCCCAAACCAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT  
CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG  
CTCAGCCTCCTGTGCTTCTGGGCCTTCTGGCCTCCTATGCAGTCATCCTCTGTCTGATAAG  
30 GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT  
ATATTTCTCATGTTTGGACCTGCTATTTTCATCTACACTTGGCCCTTCCAGGCTTTCCAGC  
TGACAAGGTAGTTTCTCTTTTCCATACTGTATCTTTCCTTTGATGAACCTGTTATTTATA  
CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG  
CTGA (SEQ ID NO: 238)

35

**AOLFR129 sequences:**

MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLFALFSVI  
YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT  
QIFLLHLLGGVEMVLLVSMADFDRYVAICKPLHYMTIMNKKVCVLLVVTSWLLGLHSGFQIPF  
40 AVNLPFCGPNVVDISIFCDLPLVTKLACIDIYFVQVVIVANSGLSLSFILLISYSLILITIKNHSPT  
GQSKARSTLTAHITVILFFGPCIFYIWPFGNHSVDKFLAVFYTIITPILNPIIYTLRNKEMKISMK  
KLWRAVNSREDT (SEQ ID NO: 239)

ATGGCTCTTTATTTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTCTCTACAGG  
45 TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAACTATTAATCAATCTCAAGTGTC  
AGAATTCATTTTGTGCTGGGACTGACCAGCTCCAGGATGTAGAGTTTCTTCTTTGCCCTCT  
TCTCGGTTATCTATGTGGTCACAGTTTTGGGTAACCTTCTTATTATAGTCACAGTGTTTAAC  
ACCCCTAACCTGAATACTCCCATGTATTTCTCCTTGGTAATCTCTCTTTGTAGATATGAC  
CCTTGCTTCTTTTGCCACCCCTAAGGTGATTCTGAACCTTGTTAAAAAGCAGAAGGTAATT  
50 TCTTTTGTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT  
ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCTACACTACATG  
ACCATCATGAACAAGAAGGTATGTGTTTGTGTTGTAGTGACCTCATGGCTCTTGGGTCTCC  
TTCACTCAGGGTTTTCAGATACCATTTGCTGTGAACCTTGCCCTTTTGTGGTCCCAATGTGGTA  
GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCCTGTATAGACATATATTTGT  
55 ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGTCTTA  
TCTCCTACAGTCTGATCCTCATAACCATTAAGAACCACTCTCCTACTGGGCAATCTAAAGC

CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTTGGCCCATGCATCTTTA  
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTATACCATC  
ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA  
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

5

**AOLFR131 sequences:**

MASTSNTLIFTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS  
LVEISYSSTIAPKFIDLLAKIKTISLEGCLTQIFFHFFGVAEILLIVVMAYDCYVAICKPLHYMNI  
ISRQLCHLLVAGSWLGGFCHSIIQLVIIQLPFCGPNVIDHYFCDLQPLFLACTDTFMEGVIVLA  
10 NSGLFSVFSFLILVSSYIVILVNLNRNHSAGRHKALSTCASHITVVILFFGPAIFLYMRPSSFTED  
KLVAVFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG  
TGCAGAGTGTATGCTTTGTGGTGTCTCTCCCGTGTACCTTGCCACGGTGGTGGGCAATGG  
15 CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA  
GCTGCCTGTCTTGGTGGAGATCAGTTATTCCTCCACTATCGCCCTAAATTCATCATAGAC  
TTACTTGCCAAGATTAAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA  
CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC  
20 ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTACCTTCTGGTGGC  
TGGTTCCTGGCTGGGGGGCTTTTGTCACTCCATAATTCAGATTCTCGTTATCATCCAATTGC  
CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT  
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTGGCCAACAGTGGATTATTCTCTG  
TCTTCTCCTTCCTCATCTTGGTGTCTCTTATATTGTCACTTCTGGTCAACTTGAGGAACCAT  
25 TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT  
TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTCACTGAAGATAAA  
CTTGTGGCTGTATTCTACACGGTCATCACCCCATGCTGAACCCCATCATTTACACACTCAG  
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA  
GGGAGTGA (SEQ ID NO: 242)

30 **AOLFR132 sequences:**

MVATNNVTEIIFVGFSQNWSEQRVISVMFLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL  
SFVEICYCSVMAPKLIFDSFIKRVISLKGCLTQMFSLHFFGGTEAFLLMVMAYDRYVAICKPL  
HYMAIMNQRMCGLLVRIAWGGGLLSVGQTFLIFQLPFCGPNIMDHYFCDVHPVLEACADT  
FFISLLIITNGGSISVVSFFVLMASYLILHLRSHNLEGQHKALSTCASHVTVDLFFIPCSLVYIR  
35 PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG  
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG  
CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGATTTCTTTCTCA  
40 GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTCATGGCCCCCAAGCTTATCTTTGAC  
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTCCCTCC  
ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGATGGCCTATGACCGCTATGTGGC  
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG  
AGGATAGCATGGGGCGGGGGCCTGCTGCATTCTGTTGGGCAAACCTTCTGATTTTCCAGC  
45 TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA  
GCTGGCCTGCGCAGACACCTTCTTCATTAGCCTGCTGATCATCACCATGGCGGCTCCATC  
TCGTAAGTCAGTTTCTTCGTGCTGATGGCTTCTACCTGATCATCCTGCACTTCTGAGAAG  
CCACAACCTTGAGGGGGCAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTACAGTTGTC  
GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAGA  
50 CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT  
TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTATTGGGGGAAAAGTAATTTGA  
(SEQ ID NO: 244)

**AOLFR133 sequences:**

55 MTEFIFLVSPNQEVQRCVFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS  
SATAPKLISDLLAERKVISWWGCMAQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN

WQVCTVLVGIAWVGGFMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLIGLLIVAN  
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI  
DKMVAVFYTVITAILNPVYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

5 ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG  
TGATATTTCTGTTCTTGTACACAGCAATTGTGCTGGGGAATTTCTCATTGTGCTCACTGTC  
ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCCTCAGCTACCTCTCCTTCATGGA  
GATCTGCTACTCCTCCGCTACAGCCCCCAAATCATCTCAGATCTGCTGGCTGAAAGGAAA  
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACTTCTTTGGTGGCACTGA  
10 GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCCTCAGC  
TACACCACCATCATGAACCTGGCAGGTGTGTACTGTCTTGTAGGAATAGCATGGGTGGGA  
GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA  
TGTGATCAATCACTATTTCTGTGACCTAGTTCCCCTTCTCAAACCTTGCTGCTGACACCT  
TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTGGGGT  
15 CCTCTTAGCATCCTATATGGTCATCTTGTCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG  
TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTCGCTGTGGTTATCTTGTCTTTGGGCCCTG  
CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCATAGACAAGATGGTGGCTGTGTTCT  
ACACAGTGATAACCGCGATCCTGAACCCTGTCTACTCTCTGAGAAATGCTGAAATGAG  
GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID  
20 NO: 246)

**AOLFR134 sequences:**

MTTILEVDNHTVTTRFILLGFPTRPAFQLFFSIFLATYLLTLENLLIILAIHSDGQLHKPMYFFL  
SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC  
25 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIQQLHYCGMPQINHYFCDISPLLNVSC  
DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSM  
LFTYARPKLMYAYNSNKVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQNGAFS  
S (SEQ ID NO: 247)

30 ATGACCACCATAATTCTGGAAGTAGATAATCATAACAGTGACAACACGTTTCATTCTTCTGG  
GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTCTCCATTTTCTGGCAACCTATCTG  
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA  
AGCCCATGTACTTCTTCTTGAGCCACCTCTCCTTCTGGAGATGTGGTATGTCACAGTCATC  
AGCCCCAAGATGCTTGTGACTTCTCAGTCATGACAAGAGTATTTCTTCAATGGCTGCA  
35 TGACTCAACTTTACTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG  
GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC  
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA  
GATGGTTTTTATAGCACAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG  
ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT  
40 CTTCTTGGCCCTCATGGTCATTGCTATTCCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA  
TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG  
TGCTCCCACCTGACCGTCGTAATTCTCTTCTATTCCATGACACTTTTACCTATGCCCGTC  
CCAACTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTACACTGTCATTGTT  
CCTCTCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA  
45 AGACCATACATTGCAGAGGAAGTGGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ  
ID NO: 248)

**AOLFR135 sequences:**

MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT  
50 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL  
AAMAYDRHAAICNPLLYSGTMSTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIIDHFFC  
DAPPLVKMSCTNTRVYEKVLGTVGFTVLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL  
ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPQ  
T (SEQ ID NO: 249)

55

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT  
 GCACCATCCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT  
 TCTATTTGGAGTGTTTCTGATGCTCTATTTGATAACCTTGTGAGGAAACATGACCTTGGTTA  
 TCTTAATCCGAACCTGATTCCCACTGCATACACCTATGTACTTTTTCATTGGCAATCTGTCT  
 5 TTTTGGATTTCTGGTATACCTCTGTGTATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA  
 AGATAAGCGCATTTCCTTGGCTGGATGTGGGGCTCAGCTGTTTTTTCCTGTGTGTAGCCT  
 AACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC  
 ATTGCTTTATTGAGGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGTGGCTCCTACA  
 TAGGAGGATTTTTGAATGCCATAGCCCATAGTCCAATACATTCCGCCTGCATTTTTGTGG  
 10 TAAAAATATCATTGACCACTTTTTCTGTGATGCACCACCATTTGGTAAAAATGTCCTGTACA  
 AACACCAGGGTCTACGAAAAAGTCTGCTTGGTGTGGTGGGCTTACAGTACTCTCCAGCA  
 TTCTTGCTATCCTGATTTCCCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT  
 TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA  
 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCCACCTACTCCCTAGAGAGGGACAAA  
 15 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG  
 AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG  
 A (SEQ ID NO: 250)

#### AOLFR136 sequences:

20 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVTVVGNLGMILLIAVSPLLHTPMYYFL  
 SSLSFVDFCYSSVITPKMLVNFLGKNTILYSECMVQLFFFVVFVAEGYLLTAMAYDRYVAIC  
 SPLLYNAMSSWVCSLLVLAFFLGLSALHTSMMKLSFCKSHIINHFCVDVPLLNLSCSNT  
 HLNELLFIHAGFNTLVPTLAVAVSYAFILYSILHRSSEGRSKAFGTCSSHLMVVFVFGSITFMY  
 FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

25 ATGACCATGGAAAATTATCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAACACAGCAAG  
 CAGAGCTCCAGCTGCCCCCTCTCCTCCTGTTCTGGGAATCTATGTGGTCACAGTAGTGGG  
 CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT  
 TCCTCAGCAGCTTGTCCTTCGTCGATTCTGCTATTCTCTGTCATTACTCCCCAAATGCTG  
 30 GTGAACTTCCTAGGAAAGAAGAATAACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT  
 TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA  
 TGTGGCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC  
 TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCCTTGACTCATAAAGTGCCATGATG  
 AAAGTGTCTTTTGCAAATCCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCCCTCCT  
 35 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTATCATTGCGGGGTTTA  
 ACACCTTGGTGCCCAACCCTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT  
 CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGAACATGCAGCTCTCATCTCATGG  
 CTGTGGTGATCTTCTTTGGGTCCATTACCTTCATGTATTTCAAGCCCCCTTCAAGTAACTCC  
 CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCTT  
 40 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA  
 AATGA (SEQ ID NO: 252)

#### AOLFR137 sequences:

MSPENQSSVSEFLLLGLPIRPEQQA VFFALFLGMYLTTVLGNLLIMLLIQLDShLHTPMYFFLSH  
 45 LALDISFSSVTPKMLNMQTQHLAVFYKGCISQTYFFIFFADLDSFLITSMA YDRYVAICHPL  
 HYATIMTQSQCVMLVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL  
 NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYYRTIIGLYFLP  
 PSSNTNDKNIIASVIYTA VTPMLNPFYISLRNKDIKGALRKLLSRGAVAHACNLSTLGG (SEQ  
 ID NO: 253)

50 ATGAGCCCTGAGAACCAGAGCAGCGTGTCGAGTTCCTCCTCCTGGGCCTCCCCATCCGGC  
 CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCTGGGCATGTACCTGACCACGGTGCTGGG  
 GAACCTGCTCATATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT  
 TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG  
 55 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTCACAGACATATT  
 TTTTCATATTTTTTGTGCTGACTTAGACAGTTTCCTTATCACTTCAATGGCATATGACAGGTAT

GTGGCCATCTGTCATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCATGC  
 TGGTGGCTGGGTCCTGGGTCATCGCTTGTGCGTGTGCTCTTTTGCATACCCTCCTCCTGGCC  
 CAGCTTTCCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGGCCCTGCT  
 CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA  
 5 GCCATTATGCTTCCATTCCCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT  
 CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA  
 GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTCTTCCCCCATCCAGCAACAC  
 CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA  
 TTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACCTTGTAGTAGG  
 10 TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

#### AOLFR138 sequences:

MLNFTDVTEFILLGLTSRREWQVLFFIVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS  
 FVDVWFSSNVTPKMLENLFSDDKTISYADCLAQCFFIALVHVEIFILAAIAFDRTYTVIGNPLLY  
 15 GSKMSRGVCIRLITFPYIYGFLTSLTATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY  
 TMLILAGINFTYSLTVIISYLFILAILMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE  
 ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTGGGGCTAACGAGCCGTCGGGAAT  
 20 GGCAAGTTCTCTTCTTCATCGTTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC  
 GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTTCTCA  
 GTCACCTGTGCTTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGaAAAT  
 CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTCTTCTTCTCAT  
 TGCTCTTGTCCATGTGGAAATTTTATTCTTGTGCGATTGCCTTTGATAGATACACAGTGA  
 25 TTGGAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGACTGATTAC  
 TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT  
 ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT  
 GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTTGCCGGCATCAACTTC  
 ACATATTCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT  
 30 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT  
 CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG  
 GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA  
 TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT  
 GTTAA (SEQ ID NO: 256)

35

#### AOLFR139 sequences:

MGFPGIHSWQHWSLPLALLYLLALSANILILIINKEAALHQPMMYYFLGILAMADIGLATTIMP  
 KILAILWFNAKTISLLECFAMQYAIHCFVAMESSTFVCMAIDRYVAICRPLRYPsiITESFVKAN  
 GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSCDDRINSINQVLLAWTLMGS  
 40 DLGLILSYALILYSVLKLNspeASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNVL  
 HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT  
 45 ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT  
 GCACCAGCCTATGTAATAATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC  
 ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG  
 AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT  
 CTGCATGGCTATTGATAGATATGTAGCCATTTGTGACCGCTACGATATCCATCAATCATC  
 ACTGAATCTTTTGTCTTCAAAGCAAATGGGTTCATGGCACTGAGAAACAGCCTGTGTCTCA  
 50 TCTCAGTGCCTCTGTTGGCTGCCAGAGGCATTACTGCTCCAGAATCAAATTGAGCACTG  
 TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT  
 AACCAGGTCCTTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTTATCAT  
 ATGCTCTAATACTTTACTCTGTCTGAAGCTGAACCTCTCCAGAAGCTGCATCCAAGGCCTT  
 AAGTACCTGCACCTCCCACCTCATCTTAATCCTTTTCTTCTACACAGTCATCATTGTGATT  
 55 CCATTACTCGTAGTACAGGAATGAGAGTTCCCCTTATTCCAGTTCTACTTAATGTGCTACA



CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAAGGAACTCAGG  
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

**AOLFR140 sequences:**

5 MLTLNKTDLPASFILNGVPGLEDTQLWISFPFCSMYVVAMVGNCGLLYLHIYEDALHKPMYY  
FLAMLSFTDLVMCSSTIPKALCIFWHLKDIGFDECLVQMFFIHTFTGMESGVLMLMALDRYV  
AICYPLRYSTILTNPVIAKVGTATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG  
NVKVNAIYGLMVALLIGGFDILCITISYTMILRAVVSLSSADARQKAFNTCTAHICAIVFSYTPAF  
10 FSFFSHRFGHEIIPPSCHIVANIYLLLPPTMNPVYGVKTKQIRDCVIRLSGSKDTSYSYM (SEQ  
ID NO: 259)

ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCCAG  
GACTGGAAGACACACAACCTCTGGATTTCCCTTCCCATTCTGCTCTATGTATGTTGTGGCTAT  
GGTAGGGAATTGTGGACTCCTCTACCTCATTCACTATGAGGATGCCCTGCACAAACCCATG  
15 TACTACTTCTTGGCCATGCTTTCCCTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA  
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTTGATGAATGCCTTGTCCAG  
ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG  
ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT  
GCAAAGGTTGGGACTGCCACCTTCTGAGAGGGGTATTACTCATTATTCCCTTTACTTTCCCT  
20 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG  
TCTGTAGCCAAATTGTCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG  
CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG  
GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCTTTAATACCTGCACTGCC  
ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTCTTTTCCACCGCTTTG  
25 GGGAAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA  
CCCACTATGAACCCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCAATA  
GGATCCTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

**AOLFR141 sequences:**

30 MSSTLGHNMESPNHTDVPDSVFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVL  
HKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFCMMESTVLLAM  
AFDRYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA  
VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC  
VILISYTPALFSFFTHRFHGHVPVHIHILLANVYLLLPALNPVVYGVKTKQIRKRVVRVFQSGQ  
35 GMGIKASE (SEQ ID NO: 261)

ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCCTTCTG  
TCTTCTTCTCCTGCGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG  
TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG  
40 AACCAGTCTTGACAAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT  
GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT  
CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTTCATGCCTTCTGCATGATGGAGTCCACT  
GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA  
CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT  
45 GCTCATGCTCCCATGTCCCTTCCCTATTGGGCGTTTGAACCTCTGCCAAAGCCATGTGATCC  
TACACACGTAAGTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA  
ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTTTTGCATTGG  
TCTCTCCTATGCCCTAAGTGCACAAGCTGTCTTCCGCTCTCATCCCATGAAGCTCGGTCCA  
AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTATCCTCATCTCTTATACACAGCCCTC  
50 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTGGC  
CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAAC  
AGATCCGTAAAAGAGTTGTCAAGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT  
CTGAGTGA (SEQ ID NO: 262)

55



**AOLFR143 sequences:**

MLGLNGTPFPQATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMYYFL  
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACL VQMFFIHTFSFMESGILLAMSLDRFVAICY  
 PLRYVTVLTHNRILAMGLGILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI  
 5 HVNNYGLLVIIFTYGMDSFILLSYALILRAMLVISQEQRLKALNTCM SHICAVLAFYVPIIAVS  
 MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPIIYSVKTKEIRKGILKFFHKSQA (SEQ ID NO:  
 263)

ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAACACTCCAGCTGACAGGCATTCCCTG  
 10 GGATACAAACAGGCCTCACCTGGGTTGCCCTGATTTTCTGCATCCTCTACATGATCTCCATT  
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTTTTGGGAGCCTGCTCTGCATCAGCCCATGT  
 ACTACTTCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCCTTTTCTACACTTCCCACT  
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCTGGTCCAGAT  
 GTTCTTCACTCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC  
 15 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG  
 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCAACCACTCTCTTCCCTTTCCCTTTTGTGGT  
 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT  
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA  
 TTTTACCTATGGTATGGACTCAACTTTTCATCCTGCTTTCTACGCATTGATCCTGAGAGCC  
 20 ATGCTGGTCATCATATCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA  
 TCTGTGCAGTGCTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG  
 AAAAGTGCTCCACCTGTTGTTTCATGTGATGATGTCCAATGTCTACCTGTTTGTACCACCCAT  
 GCTCAACCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC  
 TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

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**AOLFR144 sequences:**

MGLFNVTHPAFFLLTGIPGLESSHWSLGPCLVMY AVALGGNTVILQAVRVEPSLHEPMYYFL  
 SMLSFSDDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD  
 PLRYATVLTTEVIAAMGLGAAARSFITLFPFLFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI  
 30 NSIYGLFVLVSTFGMDLFFIFLSYVILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS  
 TVHRFGKHVPCYIHLMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

ATGGGGTTGTTCAATGTCACTCACCTGCATTCTTCTCCTGACTGGTATCCCTGGTCTGGA  
 GAGCTCTCACTCCTGGCTGTGAGGGCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA  
 35 AATACAGTGATCCTGCAGGCTGTGCGAGTGGAGCCCAGCCTCCATGAGCCCATGTACTACT  
 TCCTGTCCATGTTGTCCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC  
 CGAACCTTCTGCCTCAATGCCCCGCAACATCACTTTTGATGCCTGTCTAATTGAGATGTTTCT  
 TATCACTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG  
 TGGCCATTTGTGACCCCTTGCCTATGCAACTGTGCTCACCCTGAAGTCATTGTGCAAT  
 40 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTTCTTATTAAGA  
 GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG  
 AGGCTTGCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGATCCAC  
 CTTTGGCATGGACCTGTTTTTATCTTCTCCTCTCCTATGTGCTCATTCTGCGTTCTGTGATGG  
 CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTCACATATCCTGGC  
 45 TGTAATGCAATTTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT  
 GTCCCATGCTACATACATGTCTCATGTCAAATGTGTACCTATTTGTGCTCCTGTGCTCAA  
 CCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTTCCGCATGTTTAC  
 CACATCAAAATATGA (SEQ ID NO: 266)

**AOLFR145 sequences:**

MSVQYSLSPQFMILLSNITQFSPIFYLTSPFGLGKHWIFIPFFFMVMVAISGNCFILIIKTNPRHLH  
 TPMYYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSMESSVLLMMSFD  
 RFVAICHPLRYSVIITGQQVVRAGLIVIFRGPVATIPVLLKAFPYCGSVVLSHSFCLHQEVIQLA  
 5 CTDITFNNLYGLMVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCATHLCAVLVF  
 FVPMGLSLVHRFGKHAPPAIHLLMANVYLFVPPMLNPIIYSIKTKEIHRAIKLLGLKKASK  
 (SEQ ID NO: 267)

ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG  
 10 CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACTGGATTTTCATCC  
 CCTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG  
 ACCAACCCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT  
 GGGGCTGTGTGTGCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT  
 ATCTACTTTGGAGCGTGTCAAAATCCAGATGTTCTGCATCCACTCTTTTTCCTTCATGGAGTC  
 15 CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTTGTGGCCATCTGCCACCCCTCTGAGGTATT  
 CGGTCAATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC  
 TGTGGCCACTATCCCTATTGTCTCCTCCTGAAGGCTTTCCCTACTGTGGATCTGTGGTCC  
 TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACCACCTT  
 CAATAATCTGTATGGACTGATGGTGGTAGTTTCACTGTGATGCTGGACCTGGTGCTCATC  
 20 GCACTGTCTATGGACTCATCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC  
 GCCGTGCCTTTCAGACATGCACCGCTCATCTGTGTGCTGTGCTAGTATTCTTTGTGCCCATG  
 ATGGGGCTGTCCCTGGTGACCGTTTTGGGAAGCATGCCCCACCTGCTATTCTCTTCTAT  
 GGCCAATGTCTACCTTTTTGTGCTCCCATGCTTAACCCAATCATATACAGCATTAAGACC  
 AAGGAGATCCACCGTGCCATTATCAAACCTCCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ  
 25 ID NO: 268)

**AOLFR146 sequences:**

MSQVTNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMVFLSLM  
 LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFMSMESSVLLAMSVDYVAICCP  
 30 LHYASILTNEVIGRTGLAIICCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCAIRLN  
 SWYGFALALLIIVDPLLIVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSMT  
 HRFKHAASPLVHVIMANTYLLAPPVMNPIIYSVKNKQIQWGMNLNLSLKNMHSR (SEQ ID NO:  
 269)

ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG  
 35 GATTTGAGGCCTCCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC  
 ATGGGCAATACCACCATCCTCACTGTCAATCGCACAGAGCCATCTGTCCACCAGCGCATGT  
 ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCCCTCACCACTTACCCACA  
 GTCATGCAGCTTCTCTGGTTCAACGTTCTGATGAATCAGCTCTGAGGCCTGTTTTGCTCAGTT  
 40 TTTCTTCCTTCATGGATTCTCCTTTATGGAGTCTTCTGTCTCCTGGCTATGTCCGTTGACT  
 GCTATGTGGCCATCTGCTGTCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT  
 AGAACTGGGTTAGCCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT  
 CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCTCGTCCTATTGCCTCCACCAGGATA  
 TGATCCGCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTTGCTCTTGCCTT  
 45 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTTATTCTGAAAAATA  
 TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT  
 TCTAGCTGTCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTGCCA  
 AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT  
 GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTTAAATTTT  
 50 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

**AOLFR147 sequences:**

MPSASAMIIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYTVAVVGNLCILLYLIVVEHSLHEPMF  
 55 FFLSMLAMTDLILSTAGVPKALSIFWLGAAREITFPGLTQMFFLHYNFVLDSAILMAMAFDHYV  
 AICSPRYTTILTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI  
 NFWYGFCVPIMTVISDVILIAVSIAHILCAVFLPSQDACQKALGTCGSHVCVILMFYTPAFFSI

LAHREFGHNVSRTFHIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO: 271)

5 ATGCCATCTGCCTCTGCCATGATCATTTTTCAACCTGAGCAGTTACAATCCAGGACCCTTCAT  
TCTGGTAGGGATCCCAGGCCTGGAGCAATTCATGTGTGGATTGGAATCCCTTCTGTATC  
ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA  
GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC  
ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTTGGCTAGGGGCTCGCGAAATCACATTCC  
10 CAGGATGCCTTACACAAATGTTCTTCTTCACTATAACTTTGTCTGGATTACGCCATTCTG  
ATGGCCATGGCATTGTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATACCACCATCTT  
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC  
CTGCCAGATGTATTCTTGTGCTGACATGCCTGCCTTCTGCAGGACACGCATCATACCCACA  
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCTGTGCTGATATCTCCATCAACTTCTG  
GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCT  
15 ACGCACACATCCTCTGTGCTGTCTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT  
CGGCACCTGTGGTTCTCATGTCTGTGTCATCCTCATGTTTTATACACCTGCCTTTTTCTCCA  
TCCTCGCCCATCGCTTGGACACAATGTCTCTCGCACCTTCCACATCATGTTTGCCAATCTC  
TACATTGTTATCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA  
GAGATAAGGTTATACTTTGTTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

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**AOLFR148 sequences:**

MPTVNHSGETSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYLFLC  
MLAGADIVLSTCTIPQALAFWFRAGDISLDRCTQLFFIHSTFISESGILLVMAFDHYIAICYPLR  
YTTILTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG  
25 FSILMSTVVLDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFRG  
HIPPCIHIPLANVCILAPMLNPIHYGIKTQIQEQVVFQFLFIKQKITLV (SEQ ID NO: 273)

ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG  
30 GCCTACAGGACCAGCACATGTGGATTCTATCCCATTCCTCATTTCCTATGTACCGCCCTT  
CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT  
ACCTCTTCCTCTGCATGCTGGCTGGAGCAGACATTGTCTCTCCACGTGCACCATTCCTCAG  
GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT  
CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC  
ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCCTACAAATGCTCTGATCAA  
35 GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTCCCTATCATATTTCTTT  
TAAAAAGATTGACTTTCTGCCAGAATAATATTATTCCACACACCTTTTGTGAACACATTGG  
CCTAGCCAAATATGCATGTAATGACATTCGAATAAACATTTGGTATGGGTTTCCATTCTA  
ATGTCGACGGTGGTCTTAGATGTTGTAATAATTTTATTTTCTATATGCTGATTCTCCATGC  
TGCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTGGCTCCCATG  
40 TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTCACAATCCTTACCCAGAGGTTTGGA  
CGCCACATTCCACCTTGATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT  
GCTGAATCCCATTTATTTATGGGATCAAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT  
TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

45 **AOLFR149 sequences:**

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVLTVLGNLLILLVIRVDSHLHTTMYFLTNL  
SFIDMWFSVTVPKLLMTLVFPSGRAISFHSCMAQLYFFHFLGGTECFLYRVMSCDRYLAISSYP  
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWIQHLYCDAPPILKLACADTS  
AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEGKHRAFTCASHCIVVLCFFGPGFLFIYLR  
50 PGSRKAVDGVAVFYTVLPLLPNVVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO:  
275)

ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC  
55 TGGACGCCCCCTCTTTGGAGTCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCA  
CCAACCTGTCGTTCAATTGACATGTGGTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC

TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTTCT  
 TTCCTTCTAGGGGGCACCAGAGTGTTCCTCTACAGGGTCATGTCCTGTGATCGCTACCT  
 GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG  
 GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC  
 5 ATTTGCCCTACTGTGGACCCAACTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCCT  
 GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTTGTGACTGTTGGAATA  
 GTGGCCTCGGGCTGCTTTGTCTGATAGTGCTGTCCTATGTGTCCATCGTCTGTTCCATCCT  
 GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC  
 GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGAAAGC  
 10 TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCCCTTCTCAACCCTGTTGTGT  
 ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC  
 ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

#### AOLFR150 sequences:

15 MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTTLLGNLLIMVTVTCESRLHTPMYFLLR  
 NLAILDICFSSTAPKVLLDLLSKKKTISYTSMTQIFLFHLLGGADIFSLSVMAFDCYMAISKPL  
 HYVTIMSRGQCTALISASWMGGFVHSIVQISLLLPLFCGPNVLDTFYCDVPQVLKLTCTDTFA  
 LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGGRRKAISTCTSPHHCGDPAFCALHLCLC  
 PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

20 ATGGAGTTGGGAAATGTCACCAGAGTAAAGAATTTATATTTCTGGGACTTACTCAATCCC  
 AAGACCAGAGTTTGGTCTTGTITCTTTTTTATGTCTTGTGTACATGACGACTCTGCTGGGA  
 AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTCACACCCCCATGTACTTCCT  
 GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAAGTCTCTAAAGTCTTGC  
 25 TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT  
 CTTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTGTGATGGCGTTTACTGCTACA  
 TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT  
 CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC  
 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCCTC  
 30 AAACCTCACTGCACTGACACTTTTGTCTTGTGAGTTCTTGATGATTTCCAACAATGGCCTGGT  
 CACTACCCTGTGGTTTATCTTCCTGCTTGTGTCCTACACAGTCATCCTAATGACGCTGAGGT  
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGCACCTCCCCACATCACTGTG  
 GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC  
 AGAAAAGGCCATCTCTGTACCTTCACTGTCTCTCCCTCTGCTGAACCTTTGATCTACA  
 35 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT  
 CTGA (SEQ ID NO: 278)

#### AOLFR151 sequences:

MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYILITLAGNLCMILLIRTNSHLQTPMYFFLGHLS  
 40 FVDICYSSNVTPNMLHNFLSEQKTISYAGCFTQCLLFIALVITEFYILASMAIDRYVAICSPHYS  
 SRMSKNICVCLVTIPYMYGFLSGFSQSLTTFHLSFCGSLEINHFCADPPLMLACSDTRVKKMA  
 MFVVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFTSCASHLTIVTLFYGTLCMYVRPPSE  
 KSVEESKITAVFYTFLLSPMLNPLIYSLRNTDVILAMQQMIRGKSFHKIAV (SEQ ID NO: 279)

45 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC  
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCTTGCATCTACCTAATCACACTGGCAGG  
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATCCCACCTGCAAACACCCATGTATTTT  
 TTCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT  
 GCACAATTTCTCTCAGAACAGAGACCATCTCCTACGCTGGATGCTTACACAGTGTCTT  
 50 CTCTTCATCGCCCTGGTGATCACTGAGTTTACATCCTTGCTTCAATGGCATTGGATCGCTA  
 TGAGCCATTTGCAGCCCTTTGCATTACAGTTCAGGATGTCCAAGAACATCTGTGTCTGT  
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT  
 TCACTTATGCTTCTGTGGCTCCCTTGAATCAATCAATTTCTACTGCGCTGATCCTCTTCA  
 TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT  
 55 TAATCTCTCAAGCTCTCTCTCATCATTTCTTGTCTATCTTTTCACTTTTGCAGCGATCTT  
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCACCTGACA

ATAGTCACTTTGTTTTATGGAACCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT  
CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTGAGCCCAATGCTGAACCC  
ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA  
AAATCCTTTCATAAAATTGCAGTTTAG (SEQ ID NO: 280)

5

**AOLFR152 sequences:**

MDQINHTNVKEFFLELTRSRELEFFLVVFFAVYVATVLGNALIVVTITCESRLHTPMYFLLRN  
KSVLDIVFSSITVPKFLVDLLSDRKTISYNDCMAQIFFHFAGGADIFFLSVMAYDRYLAIKPL  
HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT  
10 FALELFMISNNGLVTLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV  
YIYCRPFMTLPMDDTTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLLGPSESRLKWG (SEQ ID  
NO: 281)

ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCTGGAACCTTACACGTTCCC  
15 GAGAGCTGGAGTTTTTCTTGTTTGTGGTCTTCTTTGCTGTGTATGTAGCAACAGTCCTGGG  
AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC  
TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCCTG  
GTGGATCTTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT  
TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC  
20 CTTGCAATCGCCAAGCCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC  
TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTGCATTCAATCATCCAGGTAATTCTGATGC  
TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCCTTCTACTGTTATGTGCTCCAGGTG  
GTAAACTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTTAACAACGGAC  
TGGTGACCCTGCTCTGGTTCCTCCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG  
25 AGATCCCACTCTGGGGAGGGGCGGAACAAAGGCCCTCTCCACGTGCACGTCCACATGCTG  
GTGGTGACTCTTCACTTCGTGCCTTGTGTTACATCTACTGCCGGCCCTTCTATGACGCTGCC  
CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCCATGCTGAACCCCATCATC  
TATTCCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG  
CCTTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

30

**AOLFR153 sequences:**

MSKTSLVTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLILLVIRVDSHLHTPMYYFLTNLS  
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSQVLAQLYFFHFLGSTECFLYTVMYSYDRYLAIKYPL  
RYTSMMSGSRCALLATSTWLSGSLHSAVQILTFLPYCGPNQIQHYLCDAPPILKLACADTSA  
35 NEMVIFVDIGLVASGCFLLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLCFFVXCVFIYLR  
PGSRDVEDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKLKRDKVAHSQGE (SEQ ID NO:  
283)

ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC  
40 TGGACGCCCCACTCTTTGGAATCTTCTGCTGGTGGTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCTCA  
CCAACCTGTCTTTCATTGACATGTGGTCTCCACTGTACGGTGCCCAAAATGCTGATGAC  
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT  
TCCACTTCTGCGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG  
45 GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG  
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT  
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCATCCTGA  
AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGGTAGT  
GGCTCGGGCTGCTTTCTCCTGATAGTGCTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC  
50 GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT  
GGTCTTTGCTTTTTTGTNNCCTGTGTTTTTCACTTACCTGAGACCAGGCTCCAGGGACGTCG  
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCCTGTTGTGTAC  
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT  
TCTCAGGGAGAATAA (SEQ ID NO: 284)

55

**AOLFR156 sequences:**

MCWAMPSPFTGSSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLLFIYTFIHDNLLIFSAVRL  
 DTHLGNPMYNFISFLEIYWYTTATIPKMLSNLISEKKAISMTGCILQMYFFHSLENSEGILLTT  
 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGFLILLPEIVMISTLPFCGPNQIHQIFCDLVP  
 5 VLSLACTDTSMLIEDVIHAVTIITFLIALSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG  
 SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPIIYSLRNKDMNNAIKKLFCLQKVLNKPGG  
 (SEQ ID NO: 285)

ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA  
 10 ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT  
 CCTGTACTTCTTTCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT  
 CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT  
 CCTTCTGGAGATCTGGTACACCACAGCCACCATTTCCCAAGATGCTCTCCAACCTCATCAG  
 TGAAGAAGAAGGCCATCTCAATGACTGGCTGCATCTTGCAGATGTATTTCTTCCACTCACTT  
 15 GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA  
 ACCCTCTTCGCTATCAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTC  
 TGCCTCTTCGGTTTCCTTATCCTGCTTCCCGAGATTGTGATGATTTCCACACTGCCTTTCTG  
 TGGGCCCCAACCAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT  
 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTCATGCTGTGACCATCATCATTACCT  
 20 TCCTAATCATTGCCCTGTCCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCTCTTCT  
 GAAGGGAGGCAAAAGGCTNTTCTACCTGTGAGGCCACCTCATGGTCTTCTGATATTCT  
 TTGGCAGTGTATCACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTGGACAC  
 AGCCATTGCACTGATGTTTACTGTACTTGCTCCATTCTCAATCCCATCATTATAGCCTGA  
 GAAACAAGGACATGAACAATGCAATTAATAAAACTGTTCTGTCTTCAAAAAGTGTGAACA  
 25 AGCCTGGAGGTAA (SEQ ID NO: 286)

**AOLFR157 sequences:**

MAMDNVTAVFQFLIGISNYPQWRDTFFTLVLIYLLSTLLGNFGMIFLIHFDPNLHTPIYFFLSNL  
 SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP  
 30 LRYSVVMNGPVCVCLVATSWGTSVLTLAMLILSLRLHFCGANVINHFACIILSLIKLTCSDTSL  
 NEFMILITSIFLLLPFGFVLLSYIRIAMAIIRISLQGRKKAFTTCGSHLTVVTFYGSISMYYMKT  
 QSKSSPDQDKFISVFYGALTPMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTTTCAGTTTCTCCTTATTGGCATTCTAAGTATCC  
 35 TCAATGGAGAGACACGTTTTTTCACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG  
 AATGGATTTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT  
 CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG  
 TGCATTGTTTCTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTC  
 TCCTTGGCTTTGGCCACAGCAGAGTGCTCCTACTGGCTGCCATGGCCTATGACCGTGTTGG  
 40 TTGCTATCAGCAATCCCTGCGTTATTCAAGTGTTATGAATGGCCCAGTGTTGTGTCTGCTT  
 GGTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG  
 CTTCACTTCTGTGGGGCTAATGTCATCAACCATTTTGCTGTGAGATTCTCTCCCTCATTA  
 GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTCAACC  
 TGCTGCTACCATTTGGGTTTGTCTCCTCTCCTACATACGAATTGCTATGGCTATCATAAGG  
 45 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG  
 TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAAACCTCAGTCCAAGTCCTCCCC  
 TGACCAGGACAAGTTTATCTCAGTGTTTATGGAGCTTTGACACCCATGTTGAACCCCTG  
 ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG  
 ACATGA (SEQ ID NO: 288)

50

**AOLFR158 sequences:**

MKAGNFSDTPEFFLLGLSGDPELQPIFLMLFLSMYLATMLGNLLIILAVNSDSLHTPMYFLLSI  
 LSLVDICFTSTTMPKMLVNIQAQAQSINYTGCLTQICFVLVFGLENGILVMMA YDRFVAJCHP  
 LRYNVIMNPKLCGLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFCELAHLKLACSDVLIN  
 55 NILVYLVTSLGVPVPLSGIIFS YTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSIFYGTGFGVYLS  
 GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKDMKALRKLISRPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAACTTCTCAGACACTCCAGAATTCCTTCTCTTGGGATTGTCAGGGGATC  
 CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCCCTGTCCATGTACCTGGCCACAATGCTGGG  
 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCCACCTCCACACCCCCATGTAATTC  
 5 TCCTCTCTATCCTGTCTTGGTCGACATCTGTTTCACCTCCACCACGATGCCCAAGATGCTG  
 GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT  
 TTGTCTCTGTTTTTGTGGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT  
 TGTGGCCATCTGTCAACCCACTGAGGTACAATGTATCATGAACCCCAAACTCTGTGGGCTG  
 CTGCTTCTGCTGTCTTCATCGTTAGTGTCTGGATGCTCTGCTGCACACGTTGATGGTGCT  
 10 ACAGCTGACCTTCTGCATAGACCTGGAAATCCCCACTTTTTCTGTGAACTAGCTCATATTC  
 TCAAGCTCGCCTGTTCTGATGTCTCATCAATAACATCCTGGTGATTTGGTGACCAGCCT  
 GTTAGGTGTTGTTCTCTCTCTGGGATCATTTTTCTTTACACACGAATTGTCTCCTCTGTCA  
 TGAATAATCCATCAGCTGGTGGAAAGTATAAAGCTTTTTCCATCTGCGGGTCACATTTAAT  
 CGTTGTTTCTTGTGTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT  
 15 CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC  
 ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG  
 GATACCATCTTCCATTGA (SEQ ID NO: 290)

#### AOLFR159 sequences:

20 MGPRNQTA VSEFLLMKV TEDPELKLIPFSLFLSMYLV TILGNLLILLA VISDSHLHTPMYFLLFN  
 LSFTDICTTTTTVPKILVNIQAQNSITYTGCLTQICLVLFAGLESCFLAVMAYDRYVAICHPL  
 RYTVLMNVHFWGLLLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKACSDTL  
 INNILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMP SARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS  
 SAVAESSRITAVASVMYTVVPQMMNPFYSLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

25 ATGGGACCCAGAAACCAAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC  
 CCAGAACTGAAGTTAATCCCTTTCAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG  
 GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCCATGTACTTC  
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAACCACAACCACAGTCCCAAAGATCCT  
 30 AGTGAACATCCAAGCTCAGAATCAGAGTACACTTACACAGGCTGCCTCACCCAGATCTGT  
 CTTGTCTTGGTTTTTGTGGCTTGGAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA  
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCTCATGAATGTCCATTTCTGGGGCTTG  
 CTGATTCTTCTCTCCATGTTCTATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT  
 GCAGCTGTCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTACAGGTC  
 35 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTTGCAAGTAGTGT  
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTTATTCTCAAATAGTCACCTCTGTTC  
 TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTCACCTCTC  
 TGTTTTTTCCTTGTTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT  
 CTCCCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC  
 40 CTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAACTTATTGGTAG  
 GCTGTTTCCTTTTTAG (SEQ ID NO: 292)

#### AOLFR160 sequences:

45 MPMQLLLTDIFIIFSIIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFLSMYLV TILGNLLILL  
 AVISDSHLHTPMYFFLSNLSFLDICTSTTTPKMLVNIQAQNSITYSGCLTQICFVLFAGLENC  
 LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLLSLLTSVNNALLSLMVLRLSFCTDLEIPLFF  
 CELAQVIQLTCSDTLNNILIYFAACIFGGVPLSGIISYQTITSCVLRMP SASGKHKA VSTCGSHL  
 SIVLLFYGAGLGVISSVVTDSPRKTA VASVMYSVFPQMVNPFYSLRNKDMKGTLRKFIGRIP  
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

50 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG  
 CATGGAAGCGAGAAACCAAACAGCTATTTCAAAATTCCTTCTCCTGGGACTGATAGAGGAT  
 CCGGAAGCTGACGCCGTCCTTTTACAGCCTGTTCTGTCCATGTACTTGGTCACCATCCTGGG  
 GAACCTGCTCATCCTCTTGGCTGTCTCTGACTCTCACCTCCACACCCCCATGTAATTC  
 55 TCCTCTCAATCTCTCTTTTGGACATTTGTTTAAGCACAACCACGATCCCAAAGATGCTG  
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCCAGATCTGCT



TTGCTTGTTTTTGGCTGGCTTGGAAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT  
 GTGGCCATTTGTACCCCCCTTAGATACACAGTCATCATGAACCCCCGCTCTGTGGCCTGC  
 TGATTCTTCTCTCTCTGTTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG  
 AGGCTGTCTTCTGCACAGACCTGGAAATCCCGCTCTTCTTCTGTGAACTGGCTCAGGTCA  
 5 TCCAACTCACCTGTTTCAAGACACCCTCATCAATAACATCCTGATATATTTTGCAGCTTGCATA  
 TTTGGTGGTGTTCCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT  
 GAGAATGCCATCAGCAAGTGGAAAGCACAAAGCAGTTCCACCTGTGGGTCTCACCTCTCC  
 ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC  
 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC  
 10 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG  
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTGAGGTTTCTAGAGTAA (SEQ ID  
 NO: 294)

#### AOLFR161 sequences:

15 MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLVMMVGNLLILLAISIDSHLHTPMYFFLANL  
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVIIAMMAYDRFVAICHPLH  
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR  
 IFILVAGMVIATPFVCLASYARILVAIMKVPSAGGRKKAFTSCSSHLSVVALFYGTTIGVYLCF  
 SSVLTTVKEKASAVMYTAVTPMLNPFYISLRNRDLKGALRKLVRNKITSSS (SEQ ID NO: 295)  
 20  
 ATGGAACCAAGAAACCAACCAAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC  
 CAGAGCAGGAGACGCTTCTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG  
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCCACCTCCACACCCCCATGTACTTCT  
 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT  
 25 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC  
 TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGT  
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCGCTG  
 CTGGTCGGCGCCCTCTGGGCGTTTTCCCTGCTTCACTCACTCACATCCTCCTGATGGC  
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC  
 30 TCCGACTTTCTGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT  
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTTGTGGCCATCA  
 TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACCTGTC  
 TGTGGTTGCTCTCTTCTATGGGACCACCATTTGGCGTCTATCTGTGTCCCTCCTCGGTCCTCA  
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC  
 35 CTTCACTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG  
 AAAGATCACCTCATCTTCCTGA (SEQ ID NO: 296)

#### AOLFR162 sequences:

40 MMRLMKEVRGRNQTEVTEFLLGLSDNPDQGVLFALFLLIYMANMVGNLGMIVLIKIDLCLH  
 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFGLGTECFLLAMMA  
 YDRYAAIWNPLLYPVLVSGRICFLLIATSLAGCGNAIHTGMTFRLSFCGSNRINHFCYDTPPL  
 LKLSGSDTHFNGIVIMAFSSFVISCVMIVLISYLCIFIAVLKMPSEGRHKAFTSCASYLMAVTIF  
 FGILFMYLRPTSSYSMEQDKVVSFYTIVIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID  
 NO: 297)  
 45  
 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC  
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTGCATTGTTTCTGTTGAT  
 CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAGATTGATCTCTGT  
 CTCCACACCCCCATGTATTTCTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT  
 50 TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG  
 GATGTGCTGCCCAGTTCTACTTCTTTGGCTCCTTCTGGGGACTGAGTGCTTCTGTTGGCC  
 ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCCTGCTCTACCCAGTTCTCGTGT  
 CTGGGAGAATTTGCTTTTTTGCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC  
 CATACTACAGGGATGACTTTTAGGTTGTCCTTTTGTGGTTCTAATAGGATCAACCATTTCT  
 55 ACTGTGACACCCCGCCACTGCTCAAACCTCTTGTCTGATACCCACTTCAATGGCATTGTG  
 ATCATGGCATTCTCAAGTTTTATTGTCATCAGCTGTGTTATGATTGTCCTCATTCTCTACCT



GTGTATCTTCATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC  
 ACCTGTGCCTCTTACCTCATGGCTGTCACCATATTCTTTGGAACAATCCTCTTCATGTACTT  
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA  
 ATAATCCCTGTGCTAAATCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC  
 5 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

**AOLFR163 sequences:**

MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVVSLTVVGNSTLIVLICNDSCLHTPMYFFTGN  
 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL  
 10 LYAQAMSIKLCALLVAVSYCGGFINSIHTKTFNFRENIDDFCDLLPLVELACGEKGGYK  
 IMMYFLLASNVICPAVLILASYLFIHTSVLRISSSKGYLKAFSTCSSHLTSVTLYYGSILYIYALPRS  
 SYSFDMDKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA  
 15 GGAATGCAGCTGGGCTCTTCGTGGTGTTCTGGGCGTGTACTCTCTCACTGTGGTAGGAA  
 ATAGCACCCTCATCGTGTTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC  
 ACTGGAATCTGTCTGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT  
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCTAGTTCTTCTCT  
 CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT  
 20 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG  
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTTCAATCATCACCAAGAAAACGTTTTTC  
 CTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTGCTTCCCTTGGTGG  
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCCCTGCTGGCCTCCAA  
 TGTCATCTGCCCCGAGTGCTCATCTGGCCTCCTACCTCTTATCATCACCAAGTGTCTTGA  
 25 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT  
 GTCACCTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT  
 TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG  
 ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAATTCTCCCATAA (SEQ  
 ID NO: 300)

30

**AOLFR164 sequences:**

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIIKINPKLHTPMYFFLN  
 HLSFVDFCYSHIAPMMLVNLVVEDRTISFSGLVQFFFFCTFVVTELILFAVMAYDHFVAICNP  
 LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHFFCELSSLISLSYPDSYL  
 35 SLLLLFTVATFNEISTLLIILTSYAFIIVTTLKMPASGHRKVFTSCASHLTAITFIHGTLFLYCVP  
 NSKNSRHTVKVASVFYTVVIPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPFNFVIEQ  
 (SEQ ID NO: 301)

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACCTCTCTTGGGCTTCTCAG  
 40 ATTACCTGGAAGTCAAATTCCTCTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG  
 GTAGGGAATCTTGGGATGATAGTGATCATCAAAATTAACCCAAAATTGCATACCCCATGT  
 ATTTTTCTCCTCAACCACCTCTCCTTTGTGGATTCTGCTATTCTCCATCATTGCTCCCATGA  
 TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT  
 CTTTTCTTTTGACCTTTGTAGTGACTGAATTAATTCTATTGCGGTGATGGCCTATGACC  
 45 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCAGAAACTCTGTGCC  
 ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG  
 CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTCTTCTGTGAGTTATCCTCC  
 CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC  
 TTTTAAATGAGATAAGCACACTACTCATCATTCTGACATCTTATGCATTCATCATTGTACCA  
 50 CCTTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCACCT  
 GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA  
 ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCTTGTGAA  
 TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT  
 AAAAAATATTTTATATTAACATAGGCATTGGTATCCATTTAATTTTGTATTGAACAATA  
 55 A (SEQ ID NO: 302)

**AOLFR165 sequences:**

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL  
 SNLSFLDICVVSSTAPKMLSIIITEQKTISFVGCATQYFVFCGMGLTECFLLAAMAYDRYAAICN  
 PLYTVLISHTLCLKMVVGAYVGGFLSSFIETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF  
 5 TSEVVTFIVSVVGVSVLVVLISYGYIVA AVVKISSATGRTKAFSTCASHL.TAVTLFYGSGFFM  
 YMRPSSSYSLNRDKVVSIFYALVIPVVPNIYTSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG  
 (SEQ ID NO: 303)

ATGGCTGTAGGAAGGAACAACAATTGTGACAAAATTCATTCTCCTGGGACTTTCAGACC  
 10 ATCCTCAAATGAAGATTTTCCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC  
 TGGAACCTTAAGCCTCATTGCCCTCATTAAAGATGGACTCTCACCTGCACATGCCCATGTACT  
 TCTTCCTCAGTAACCTGTCCTTCCTGGACATCTGCTATGTGTCCTCCACCGCCCCTAAGATG  
 CTGTCTGACATCATCACAGAGCAGAAAACCAATTCCTTTGTTGGCTGTGCCACTCAGTACT  
 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG  
 15 GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATACACTTTGTTTAA  
 AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTAGTTCTTTTCATTGAAACATACTCTGT  
 CTATCAGCATGATTTCTGTGGGCCCTATGATGATCAACCACTTTTCTGTGACCTCCCTCCAG  
 TCCTGGCTCTGTCTGCTCTGATACCTTCACCAGCGAGGTGGTGACCTTCATAGTCAGTGTT  
 GTCGTTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGCTGT  
 20 TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG  
 ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCAGCTA  
 CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCCGTGGTGAAT  
 CCCATCATCTACAGTTTTAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA  
 AGGGACCCCGGGATTTCTCACGGTGGACCATTCATTTTATGACCTTGGGCTAA (SEQ ID  
 25 NO: 304)

**AOLFR166 sequences:**

MEMENCTRVKEFIFLGLTQNREVSLLVFLFLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH  
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGGVDFVSLVSMALDRYVAISKPL  
 30 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLPLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL  
 ELLMISNNGLLTTLWFFLLLVSYIVLSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIVYARP  
 FTALPMDKAISVTFVVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

ATGGAGATGGAAACTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC  
 35 GGGAAGTGAGCTTAGTCTTATTTCTTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA  
 AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTTT  
 GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTCCATCACAGTGCCCAAGGTTCTGG  
 TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA  
 TTCCACCTTATTGGAGGGGTGGATGTATTTCTCTTTCGGTGATGGCATTGGATCGATATG  
 40 TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT  
 CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGCAGATTCCCTGTTGCTC  
 CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCCT  
 CAAACTGGCCCATACAGACATTTTCATACTTGAACCTACTAATGATTCCAACAATGGACTG  
 CTCACCACACTGTGGTTTTTCTGCTCCTGCTGCTACATAGTCATATTATCATTACCCAA  
 45 GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACTGT  
 GGTGACCCTGCATTTCTGTCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCA  
 TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCCTCTGCTCAACCCCTTGATCTAC  
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT  
 TCTGATAGAAAATAG \*SEQ ID NO: 306)

50

**AOLFR167 sequences:**

MSITKAWNSSSVTMFILLGFTDHPQLQALLFVTFGLGIYLTTLAWNLAFLIRGDTHLHTPMYFF  
 LSNSFLIDICYSSAVAPNMLTDFWEQKTISFVGCAAQFFFFVGMGLSECLLLTAMAYDRYAAI  
 SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFCGPNIIHFFCDLPPVLALSCSDT  
 55 FLSQVNVNLFVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTTLLFGTAL

FVYLRPSSSYLLGRDKVVSFVYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID NO: 307)

5 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA  
CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC  
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA  
TGTACTTCTTCCTAAGCAACTTATCTTTTCATTGACATCTGCTACTCTTCTGCTGTGGCTCCC  
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTGTGGGCTGTGCTGCTC  
10 AGTTTTTTTTCTTTGTGCGCATGGGTCTGTCTGAGTGCCTCCTCCTGACTGCTATGGCATA  
GACCGATATGCAGCCATCTCCAGCCCCCTTCTCTACCCCACTATCATGACCCAGGGCCTCT  
GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCCTGAGCTCCCTGATCCAGGCCAG  
CTCCATATTTAGGCTTCACTTTTGCGGACCCAACATCATCAACCACTTCTTCTGCGACCTCC  
CACCAGTCTGGCTCTGTCTTGCTCTGACACCTTCCTCAGTCAAGTGGTGAATTCCTCGTG  
15 GTGGTCACTGTCGGAGGAACATCGTTTCTCCAACTCCTTATCTCCTATGGTTACATAGTGT  
CTGCGGTCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT  
CGCATCTGATGGTGGTGAATCTGTCTGTTTGGGACAGCCCTTTTCGTGTAATTCGCGACCCAG  
CTCCAGCTACTTGCTAGGCAGGGACAAGGTGGTGTCTGTTTCTATTGATGGTGTATCCCC  
ATGCTGAACCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG  
GTGTTGGAAAGGAAGAAAGTGTTCCTTAG (SEQ ID NO: 308)

20

**AOLFR168 sequences:**

MEKINNVTETEFWGLSQSPEIEKVCFVVSFFYIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV  
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAYDRYVAICKPLHYM  
25 TIMNRETCNKMLLGTWVGFLHSIIQVALVVQLPFCGPNEIDHYFCDVHPVLKLACTETIYIVG  
VVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD  
TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

30 ATGGAAAAATAAAACAACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA  
TTGAGAAAGTTTGTGTTTGTGGTGTTCCTTTCTTCTACATAATCATTCTTCTGGGAAATCTC  
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTTCTTTCTCAG  
CTTCTTGCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC  
TGTTAGCAAAGGACAAAACCATCTCCTTATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC  
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT  
35 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT  
TAGGGACGTGGGTAGGTGGGTTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAAC  
ACCTTTTGTGGACCCAATGAGATAGATCACTACTTTTGTGATGTTACCCCTGTGTTGAAA  
CTTGCCTGCACAGAAACATACATTGTGTTGTTGTTGTGACAGCCAACAGTGGTACCATTG  
CTCTGGGGAGTTTTGTTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG  
40 CAGTCAGCAGAAGGCAGGCGCAAAGCCCTCTCCACCTGTGGCTCCACATTGCCATGGTCG  
TTATCTTTTTCGGCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT  
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTAAATCCTCTGATTTATACACT  
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTTCTTGGA  
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

45

**AOLFR169 sequences:**

MMDNHSSATEFHLLGFPQSQGLHHILFAIFFFFYLVTLMGNTVIIIVCVDKRLQSPMYFFLSHL  
STLEILVTIIVPMMMLWGLLFLGCRQYLSLHVSINFSCGTMEFALLGVMAVDYVAVCNPLRY  
NIIMNSSTCIWVIVSWVFGFLSEIWIPIATFQFTFRKSNSLDHFYCDRGQLKLSCDNTLLTEFI  
50 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRKAFSTFASHFTCVVIGYGSCFLYVVKPKQTQ  
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

55 ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG  
GACTACACCACATTCTTTTGTCTATATTCTTTTCTTCTATTTAGTGACATTAATGGGAAAC  
ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCTCCT  
CAGCCACCTCTCTACCCTGGAGATCCTGGTCAACAACATAATTGTCCCCATGATGCTTTGG

GGATTGCTCTTCCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCCTG  
 TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT  
 AACCCCTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT  
 CATGGGTGTTTGGATTCTTTCTGAAATCTGGCCCATCTATGCCACATTTACGTTTACCTTC  
 5 CGCAAATCAAATTCATTAGACCATTTTACTGTGACCGAGGGCAATTGCTCAAACGTGCTCT  
 GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT  
 TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC  
 AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTCACCTGTGTTGTGATTG  
 GCTATGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACACAGGGAGTTGAGTACAA  
 10 TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCTGAATCCTTTTCTCTTTACTCT  
 TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT  
 GAAAGATTAG (SEQ ID NO: 312)

#### AOLFR170 sequences:

15 MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCLYLSVS  
 ASPSVFCFSQMGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIIVMVI  
 ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLLVPHKVITFTGCMVQFYFHFSLGSTSFLIL  
 TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH  
 FFCNEPLLQLSCSDTRLLEFWDFLMALTFVLSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG  
 20 SHLTLVFIGYSTIFLYVRPGKAHSVQVRKVVALVTSVLTPLNPFILTFCNQTVKTVLQGMQ  
 RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACTTCTCTCATACCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT  
 TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTACTTGCCTTT  
 25 CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTTCTCTGTCTC  
 TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTTCTCTTGATGCAGGGCCCATACTG  
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCCTCTTGGGCTTCTCCTCCTTTGG  
 TGAGCTGCAGGCCCTTCTGTATGGCCCCCTTCTCATGCTTTATCTTCTCGCCTTCATGGGAA  
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC  
 30 CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCAGGATGCTCT  
 CAGACCTGTTGGTCCCCCACAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC  
 CACTTTTCCCTGGGGTCCACCTCCTTCTCATCCTGACAGACATGGCCCTTGATCGCTTTGT  
 GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG  
 GCTGGGGCTGCCTGGGCAGCTCCTTTCTAGCCATGGTACCCACTGTCCTCTCCCGAGCTC  
 35 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG  
 CAGTTGTGATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT  
 TGTCTCAGCTCCTTCTGCTGACCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC  
 GGATCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGCGGGTCTCACCTCACACT  
 GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT  
 40 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCCTTTCTCAATCCCT  
 TTATCCTTACCTTCTGCAATCAGACAGTTAAAACAGTGCTACAGGGGCAGATGCAGAGGCT  
 GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

#### AOLFR171 sequences:

45 MVGNLLIIVTTIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLLCDKIAISLSACMGQLFI  
 EHLLGGAEVFLLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVMIGGFVHSVQIVFLYSLP  
 ICGPNVIDHSVCDMYPLLELLCLDTYFIGLTVVANGGHCIMVIFTLLISCGVILNFKTYSQEER  
 HKALPTCISHIIVVALVFVPCIFMYVRPVSNNFPDKLMTVFYSIITLMLNPLIYSLRQSEMKNAM  
 KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

50 ATGGTGGGAAACCTCCTCATTGTTGGGTGACTACTATTGGCAGCCCCCTCCTTGGGCTCCCTAA  
 TGTACTTCTTCCCTGCCTACTTGTCACTTATGGATGCCATATATCCACTGCCATGTCACCC  
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC  
 AGCTCTTCATAGAACACTTACTTGGTGGTGAGAGGTCTTCTTTTGGTGGTGATGGCCTA  
 55 TGATCGCTATGTGGCTATCTTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT  
 TGCATCCTTCTGTTGGTGGTGCCATGATTGGAGGTTTGTGCACTCTGTGGTTCAAATTGT

CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT  
 ACCCATTTGTTGGAACCTGTTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA  
 TGGTGGAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA  
 ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA  
 5 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTTATGTATGTTAGACCCGTTTCCA  
 ACTTTCCCTTTGATAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT  
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA  
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCCACTGAACATATTTATTCTAGTTCTA  
 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

10

**AOLFR172 sequences:**

MAETLQLNSTFLHPNFILTGFPGLGSAQTWLTTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM  
 FLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR  
 AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFLLVAKFEHFQAKTIGHTYCAHMAV  
 15 VELVVGNTQATNLYGLALSLAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSHICVIL  
 AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPALNPLIYGARTKQIRDRLLETFTFRKSPL  
 (SEQ ID NO: 317)

ATGGCAGAAACTCTACAACCTCAATTCCACCTTCCTACACCCAAACTTCTTCATACTGACTG  
 20 GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCATTATCT  
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA  
 CCAGCCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT  
 ATAGCCCCAGGGTTGCTGGCTGTGCTTGGGCCCCGATCTGTGCCATATGCTGTGT  
 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC  
 25 CATGGCCTGTGATCGTGTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCTGGTCACC  
 AAAGCCTGTGTGGGTTATGCAGCCTTGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC  
 CTTTCCCACTGCTGGTGGCAAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA  
 TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA  
 TGGTCTGGCACTTTCAGTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT  
 30 GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG  
 GTACATGTAGTTCTCACATCTGTGTCATTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC  
 CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCAACAT  
 CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCCGCACCAAGCAGATC  
 AGAGACCGACTCCTGGAAACCTTCACATTGAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

35

**AOLFR173 sequences:**

MSHTNVTIFHPAVFVLPPIGLEAYHIWLSIPLCLIYITAVLGNSILIVVIVMERNLHVPMYFFLS  
 MLAVMDILLSTTTVPKALAIFWLQAHNIAFDACVTQGGFFVHMMFVGESAILLAMAFDRFVAIC  
 APLRYTTVLTPVVGRIALAVITRSFCIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV  
 40 NIWYGFSPVIVMVILDVILAVSYSLILRAVFRLPQDARHKALSTCGSHLCVILMFYVPSFFTL  
 THHFGNRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREGVAHRFFDIKTWCCTSPLGS  
 (SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTGGCATCCCTGG  
 45 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTGCCTCATTTACATCACTGCAGTCC  
 TGGGAAACAGCATCCTGATAGTGGTTATTGTCATGGAACGTAACCTTCATGTGCCCATGTA  
 TTTCTTCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG  
 CCTAGCCATCTTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTACCCAAAGGC  
 TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG  
 50 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG  
 AGGATTGCTCTGGCCGTCATCACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT  
 GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCCCTCACTCCTACTGTGAGCATATTGGA  
 GTGGCTCGTTTAGCCTGTGCTGACATCACTGTTAACATTGGGTATGGCTTCTCAGTGCCCAT  
 TGTGATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG  
 55 TGTTTCGTTTGGCCTCCAGGATGCTCGGCACAAGGCCCTCAGCACTGTGGCTCCACCT  
 CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG

TAATATTCCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTGGCAGTGCCACCAATGC  
TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGGTGTAGCCCACCGTT  
CTTTGACATCAAGACTTGGTGTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

5 **AOLFR175 sequences:**

MHFLSQNDLNINLPHLCLHRHSVIAGAFTHRHMKIFNSPNSSTFTGFILLGFPCPREGQILLFV  
LFTVVYLLTLMGNNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF  
SGCFLQFYFFFSLSGTECFLLAVMAFDRLAICRPLRYPTIMTRRLCTNLVNCWVVLGFIWFLPI  
VNISQMSFCGSRIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVVRAVL  
10 RVPSAAGRRKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLNPVI  
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG  
TCATTCAGTAATTGCTGGTGCTTTTACAATTCACAGGCACATGAAAATCTTCAACAGCCCC  
15 AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC  
AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCTCATGGGCAATGGTTCC  
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA  
ACTTCTCCTTCTTGGAGATATGTTATGTCACCTCCACAGTCCCCAGCATGCTGGCCAACTTC  
CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCTCCAGTTCTACTTTTTCTTCTCC  
20 TTGGGCTCTACAGAATGCTTTTTCTGCGCAGTTATGGCATTGATCGATACCTTGCCATCTG  
TCGGCCTCTACGCTATCCAACCATATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT  
GCTGGGTACTTGGTTTCATCTGGTTCTTGATTCTATCGTCAACATCTCCCAAATGTCCTTC  
TGTGGATCTAGGATTATTGACCACTTCCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG  
CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTCTGTTCTTAAGTCTCTGCCTGTCTTTATGC  
25 TCTTCTCTTCAATTGTGGGGTCTATGCTCTGGTCTGAGAGCTGTGTTGAGGGTCCCTTCA  
GCAGCTGGGAGAAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT  
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCCAACATCTAAGAATGAAGCTGGAAAGC  
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCCACTGCTTAACCTGTGATATATAGT  
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:  
30 322)

**AOLFR176 sequences:**

MFFIIHSLVTSVFLTALGPQNRTHMFVTEFVLLGFHGGQREMQSCFFSFILVLYLLTLLGNGAIVC  
AVKLDRLRLHTPMYILLGNFAFLEIWYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLSGTTTECF  
35 LSV MAYDRYLAICRPLHYPSIMTGKFCILVCVCWVGGFLCYPVPIVLISQLPFCGPNIDHLVCD  
PGPLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV  
VSLFYGTLVMVYVSPTSGNPAGMQKIITLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGLTVS  
QN (SEQ ID NO: 323)

ATGTTCTTTATTATTCACTTCTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCCAGAA  
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG  
CAGAGCTGCTTCTTCTCACTCATCCTGGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC  
TATTGTCTGTGCACTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA  
AACTTTGCCTTTCTAGAGATCTGGTACATTTCTCCTCACTGTCCCAAACATGCTAGTCAATAT  
45 CCTCTCTGAGATTAACCATCTCCTTCTCTGGTTGCTTCTGCAATTCTATTTCTTTTTTCT  
ACTGGGTACAACAGAGTGTTTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC  
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT  
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTTCCCT  
TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCAATTGTTTGCAGTGGC  
50 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG  
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC  
TCTGGTGTGGTGAACCTAAAGCTTTCTCCACATGTGGGTCCCACCTAATGGTGGTGTCTC  
TATTCTATGGAACCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT  
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCCTTATCTAT  
55 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTGGGGTTAACAGTTAGC  
CAAACTGA (SEQ ID NO: 324)

**AOLFR177 sequences:**

MSFFFVDLRPMNRSATHIVTEFILLGFPGCWKIQIFLSLFLVIYVLTLLGNGAIIYAVRCNPLLH  
 TPMYFLLGNFALEIWYVSSSTIPNMLVNILSKTKAISFSGCFLQFYFFSLGTTECLFLAVMAYD  
 5 RYLAICHPLQYPAIMTVRFCKGLVSFCWLIGFLGYPIFYISQLPFCGPNIDHFLCDMDPLMAL  
 SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLLTAVFQVPSAAGRRAKAFSTCGSHLVVVSIFYG  
 TVMVMYVSPTYGIPTLLQKILTLVYSVTTPLFNPLIYTLRNKDMKLALRNVLFGMRIRQNS  
 (SEQ ID NO: 325)

10 ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG  
 AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAGATTCAGATTTTCTCTTCTCATTGTTT  
 TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA  
 ACCCACTACTACACACCCCATGTACTTCTGCTGGGAAATTTTGCCTTCTTGAGATCTGG  
 TATGTGTCTCCACTATTCCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC  
 15 ATTTTCTGGGTGCTTCCCTCCAGTTCTATTTCTTCTTTTCACTGGGAACAACTGAATGTCTCT  
 TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC  
 CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCCCTG  
 GATACCAATTCCCATTTTCTACATCTCCCAACTCCCCTTCTGTGGTCCCTAATATCATTGAT  
 CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCATAACTG  
 20 AATGTATTTTCTATACTCAGAGCTCCCTTGCTCTTTTCTACTAGTATGTACATTCTTCGA  
 TCCTATATCCTGTTACTAACAGCTGTTTTTCAGGTCCCTTCTGCAGCTGGTCGGAGAAAAG  
 CCTTCTCTACCTGTGGTTCTCATTTGGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA  
 ATGTATGTAAGTCCTACATATGGGATCCCAACTTATTGCAGAAGATCCTCACACTGGTAT  
 ATTCAGTAACGACTCCTCTTTTAACTCTGATCTATACTCTTCGTAATAAGGACATGAAA  
 25 CTCGCTCTGAGAAATGTCTGTTTGAATGAGAATTCGTCAAATTCGTGA (SEQ ID NO:  
 326)

**AOLFR178 sequences:**

MVGANHSVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL  
 30 ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP  
 LQYLTIMSPRMCMFFLVAAWVTGLIHSVVLVFNLPFCGPNVSDSFYCDLPRFIKLACTDSY  
 RLEFMVTANSFISLGSFFILIISYVVIITVLKHSSAGLSKALSTLSAHVSVVVLFFGPLIFVYTW  
 PSPSTHLDKFLAIFDAVLTPVLNPIIYTFRN (SEQ ID NO: 327)

35 ATGGTTGGGGCAAATCACTCCGTGGTGTGAGAGTTTGTGTTCTCTGGGACTACCAATTCCT  
 GGGAGATCCGACTTCTCCTCCTTGTTCTCTCCATGTTTTACATGGCCAGTATGATGGGA  
 AACTCTCTCATTTTGCTCACTGTGACTTCTGACCCTCACTTGCCTCCCCATGTATTTTCT  
 GTAGCCAACTCTCCTTCATTGACCTGGGTGTTTCTCTGTCACTTCTCCCAAATGATTT  
 ATGACCTGTTGAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT  
 40 CATCCACGTCATTGGCGGTGTGGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAT  
 GTGGCCATATGTAAGCCCCTCCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT  
 TCTTAGTGGCTGCCTGGGTGACCGGCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA  
 AACTTGCCCTTCTGTGGTCTAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCAT  
 CAAACTTGCTGCACAGACAGCTACCGACTGGAGTTTCATGGTTACAGCCAACAGTGGATTCT  
 45 ATCTCTCTGGGCTCCTTCTTCACTGATCATTTCTATGTGGTCATCATTCTCACTGTTCT  
 GAAACACTCTTCAGCTGGTTTATCCAAGGCTCTGTCCACCCTTTCAGCTCACGTCAGTGTG  
 GTAGTTTTGTCTTTGGTCTTTGATTTTGTCTATACGTGGCCATCTCCCTCCACACACCT  
 GGATAAGTTTCTGGCCATCTTTGATGCAGTTCTCACTCCTGTTTTAAATCCTATCATCTACA  
 CATTCAGGAATTGA (SEQ ID NO: 328)

50

**AOLFR179 sequences:**

MNGMNHSVSEFVFMGLTNSREIQLLLFVFSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL  
 ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP  
 LHYLTIMSPRMCLYFLATSSIIHLIHSVLVQVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL  
 55 EFMVTVNSGLISVGSFVLLVISYIFILFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW  
 PSPTSHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFTKIL (SEQ ID NO: 329)



ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTTCATGGGACTCACCAACTCAC  
 GGGAGATTTCAGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA  
 AACCTTGTCAATTGTATTCACTGTAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCT  
 5 CCTGGCTAACCTCTCAATCATTGATATGGCATTGCTCAATTACAGCCCCCTAAGATGATT  
 GTGATATTTTCAAGAAGCACAAGGCCATCTCCTTTTCGGGGATGTATTACTCAGATCTTCTT  
 TAGCCATGCTCTTGGGGGCACTGAGATGGTGTCTCATAGCCATGGCCTTTGACAGATAC  
 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT  
 TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA  
 10 GATTACCTTTTTGTGGTCCTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT  
 CAGACTTGCCTGTACCAACACCCAAGAACTGGAGTTCATGGTCACTGTCAATAGTGGACTC  
 ATTTCTGTGGGCTCCTTTGTCTTGCTGGTAATTTCTACATCTTCATTCTGTTCACTGTTTG  
 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCCTGTCAGCTCATGTCACTGTG  
 GTCATCTTGTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCACATCACACCT  
 15 GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA  
 CATTACAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT  
 TTACAAAGATTTTGTAA (SEQ ID NO: 330)

**AOLFR180 sequences:**

20 MTNKMAYAIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSNFLLTAFPGLECAHVWISIPVCCLYTI  
 ALLGNMIFLVIITKRRLHKPMYYFLSMLAAVDLCLTITLPTVLGVLWFHAREISFKACFIQMF  
 FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRLVGLVICIRPAVFLPLLVAINTVSF  
 HGGHELHPFCYHPEVIKYTYSKPWISSFWGLFLQLYLNGTDVLFILFSYVLILRTVLGIVARKK  
 QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLLPPVLNPIIYSLKTKTIR  
 25 QAMFQLLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTTCTTTCCTCATAGT  
 TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCTCAAACCTTCC  
 TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT  
 30 CTCTACACCATTTGCCCTCTTGGGAAACAGTATGATCTTCTTGTTCATCATTACTAAGCGGA  
 GACTCCACAAACCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC  
 ATTACGACCCTTCCCACTGTGCTTGGTGTCTCTGGTTTCATGCCCGGAGATCAGCTTTAA  
 AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCCCTCGGTGCTGG  
 TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC  
 35 ACAGACAGGATGGTCTCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTTCTTAC  
 TTCCCCTTCTTGTAGCCATAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA  
 TTTTGCTACCAACCCAGAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT  
 GGGGACTGTTTCTTCACTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTCTCCTAT  
 GTCCTGATCCTCCGTACTGTTCTGGGCATTGTGGCCCCGAAAGAAGCAACAAAAAGCTCTCA  
 40 GCACITGTGTCTGCACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT  
 TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGCTCTGTAGCACTTTGGCCAATATTTA  
 TCTGCTCTTACCACCTGTGCTGAACCTATCATTTACAGCTTGAAGACCAAGACAATCCGC  
 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTTAATGTGAGGGGTCTTA  
 GGGGAAGATGGGATTGA (SEQ ID NO: 332)

45

**AOLFR181 sequences:**

MSVLNNSEVKLFLLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMMYYFLAML  
 AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR  
 YSSILTSNRVAKMGLILAIRSILLVFPFPTLRRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNR  
 50 IYGFIALCTMLDLALIVLSYVLILKILSLASLAERLKALNTCVSHICAVLTFYVPIITLAAMHHF  
 AKHKSPVLVILIADMFLLVPLMNPIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTCTGATTGGGATCCCAGGACTGG  
 AACATGCCACATTTGGTTCTCCATCCCCATTTGCCCTCATGTACCTGCTTGCCATCATGGGC  
 55 AACTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT  
 CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCTACCATGTTGA



GGGTCTTCTTGTTCATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATTCTTC  
 ATTCATGGATTCACTGTCATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT  
 TGCCATTACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAAATG  
 GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTCACCTTAAGGAG  
 5 ATTAATAATTGTCAAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA  
 AGCTGGCCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCATTGCTCTCTGTACT  
 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT  
 TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCACATCTGTGCTGTG  
 CTCACCTTCTATGTGCCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA  
 10 GCCCTCTTGTGTGATCCTTATTGCAGATATGTTCTTGTGGTGCCGCCCTTATGAACCCC  
 ATTGCTGACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTGGGGAAGTTGCTTAAT  
 GTATGTGGGAGATAA (SEQ ID NO: 334)

#### AOLFR182 sequences:

15 MTLGSLGNSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYLFL  
 SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP  
 LHYVSILTNTVIGRIGLVSIGRSVALIFPLPFMLKRFPYCGSPVLSHSYCLHQEVMLACADMK  
 ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV  
 IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVYSVKTKQIRDRVTHAFY (SEQ ID NO: 335)  
 20  
 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCCTGCTGAGTG  
 GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT  
 GGTTTCCATCCCGGGCAACTGCACAATTCTTTTTATCATTAACAGAGCGCTCACTTCAT  
 GAACCTATGTATCTCTTCCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTCAC  
 25 TCTCCCTACAGTCTGGGCATCTTTTGGGTGGAGCAGAGAAATTAGCCATGATGCCTGC  
 TTTGCTCAGCTCTTTTTCATTCACTGCTTCTCCTTCCTCGAGTCTCTGTGCTACTGTCTATG  
 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC  
 AGTCATTGGCAGGATTGGCTGGTCTCTCTGGGTCTGTAGTGTAGCACTCATTTTTCCATTA  
 CCTTTTATGCTCAAAAGATTCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT  
 30 CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT  
 GTTTGTCATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA  
 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG  
 TGTTCACCATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCTATCC  
 ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTCATGGGTTTTCATGTATCTTCT  
 35 CTTCTCCTGTGATGAATCCCATTGTCTACAGTGTGAAGACCAACAGATCCGGGATCGA  
 GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

#### AOLFR183 sequences:

MTNLNASQANHRNFILTGIPGTPDKNPWLAFLPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYFYL  
 40 SILALTDVSLSMSTLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGVLVSMAFDRFVAIRN  
 PLHYVSILTHDVIRKGTGISVLTRA VCVFPVPFLIKCLPFCHSNVLSHSYCLHQNMRLACASTR  
 INSLYGLIVVIFTLGLDVLLTLLSYVLTLKTVLGIVSRGERLKLSTCLSHMSTVLLFYVPMGA  
 ASMIHRFWEHLSPVVMVMDIYLLPVLNPVYSVKTKQI (SEQ ID NO: 337)  
 45  
 ATGACGAACTGAATGCATCACAGGCCAACACCCTAACTTCATTCTGACAGGTATCCAG  
 GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCTGGGATTTCTCTACACACTCACACT  
 CCTGGGAAATGGTACCATCCTAGCTGTCATCAAGGTGGAGCCAAGTCTCCATGAGCCCACG  
 TATTACTTCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC  
 ATGCTCAGCATCTACTGGTTAATGCCCTCAGATTGTTTTGATGCATGCATCATGCAGAT  
 50 GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCTAGTGTCCATGGCCTTTGAC  
 AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTGG  
 AAAGACTGGAATATCTGTCTCACCCGGGAGTCTGTGTGGTATTCCCTGTGCCCTTCTT  
 ATAAAGTGCCTACCCTTCTGCCATTCCAATGTCTTGTCTCATTCACTGTCTTACCAAAA  
 CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC  
 55 ATCTTCACACTGGGGCTCGATGTTCTCCTCACTCTACTGTCTTATGTACTCACCTGAAGAC  
 TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAACCCCTCAGCACATGCCTCTCTCAC

ATGTCTACCGTGCTCCTCTTCTATGTTCCCTTTATGGGTGCTGCCTCCATGATCCACAGATT  
TTGGGAGCATTTATCACCAGTAGTGCACATGGTCATGGCTGATATATACCTACTGCTCCCG  
CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

5 **AOLFR184 sequences:**

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPLIAVYLLSALGNGTILWIALQPALHR  
PMHFFLFLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFHVSVMESSVLLAMSID  
RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLLAYMPYCLPQVLTHSYCLHPDVARL  
ACPEAWGAAYSFLFVLSAMGLDPLLFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF  
10 YIPMILLALINHPelpITQHTHTLLSYVHFLPLPLNPILYSVKMKEIRKRLNRLQPRKVGGAGQ  
(SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT  
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATTGC  
15 TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC  
GCCCTGCACCGCCCAATGCACTTCTTCCTCTTCTTGCTTAGTGTGTCTGATATTGGATTGGT  
CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTTGCTGGTGCTCACACTGTCCCTGCC  
TCAGCCTGCCTTCTACAGATGGTTTTATCCATGTCTTTCTGTCTGAGTCCCTCTGTCTT  
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC  
20 CTCACCAATGGTGTAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC  
ATCTGCCCCTGCCATTCTGTGCTGGCTACATGCCCTACTGCCCTCCACAGGTCTTAACCCAT  
TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCCAGAAGCTTGGGGTGCAGCCT  
ACAGCCTATTTGTGGTTCTTTACGCCATGGGTTTGGACCCCCTGCTTATTTCTTCTCCTAT  
GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT  
25 CAAACCTGTGCTGCCACCTCTCTGCAGTGTCTCTCTATATCCCTATGATCCTCCTGGC  
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTATCCTATCTGTC  
ATTTCTTCTTCTCCTCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA  
AAGAGAACTACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGCTCAGTGA (SEQ ID NO:  
340)

30

**AOLFR185 sequences:**

MFYPILNDISTKNNSNIMSCCNILFIKTVEIILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR  
VDCVPSRDHINQSMVLASGNSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR  
IDHTLHEPMYFLAMLAITDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESGVL  
35 MAMALDCYVATCFPLRHSSILTPSVVIKLGITVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC  
EHMAVLKLVCAOTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA  
SHICVILALYIPALFSFLTYRFGHDVPRVVHILFANLYLLIPMLNPIIYGVRTKQIGDRVIQGCCG  
NIP (SEQ ID NO: 341)

40 ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTGTCATGTT  
GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC  
CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAATAACACTTGTTTTGATTGTT  
ATCATCTGCAGAGAGTAGATTGCGTTCCCAGCAGAGACCATATTAACAGTCCATGGTGCT  
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTTCATCCTGCTTGGAATCCCAGGCCTG  
45 GAGAGTTTCCAGTTGTGGATTGCCTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG  
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC  
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCCTCCTCACTCAACCTAAGATGTT  
GGCCATATTCTGGTTTCATGCTCATGAGATTGAGTACCATGCCTGCCTCATCCAGGTGTTCT  
TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC  
50 GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTGCTGATCAAAC  
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCCCTTCTGCTTCATGGTGTC  
TAGGATGCCCTTCTGCCAACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG  
CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT  
CTGTGGCTGGCTTTGATATGATTGTGATTGGTATGTACATCGTGATGATTTTGAGAGCTGT  
55 GCTTCAGTTGCCCTCAGGTGAAGCCCGCCTCAAAGCTTTAGCACACGTGCCCTCCCATATC  
TGTGTCATCTTGGCTCTTTATATCCAGCCCTTTTCTTCTCCTCACCTACCGCTTTGGCCAT

GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT  
CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG  
TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

5 **AOLFR186 sequences:**

MSNASLVTAFILTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS  
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL  
RYTSMMSGSRCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTSA  
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRIRTS DGRRRAFQTCASHCIVVLCFFVPCVVIYLR  
10 PGSM DAMDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKL RDKVAHPQRK (SEQ ID NO:  
343)

ATGTCCAACGCCAGCCTCGTGACAGCATTCATCCTCACAGGCCTTCCCCATGCCCCAGGGC  
TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
15 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCA  
CCAACCTGTCCCTCATTGACATGTGGTTCTCCACTGTCACGGTGCCAAAATGCTGATGAC  
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT  
TCCACTTCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACTTG  
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG  
20 CCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT  
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA  
AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT  
GGCCTCAGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCATCCTGC  
GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT  
25 GGTCTTTGCTTCTTTGTTCCTGTGTTGTCTATTATCTGAGGCCAGGCTCCATGGATGCCA  
TGGATGGAGTTGTGGCCATTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGTAC  
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAACTTAGAGACAAAGTAGCACAT  
CCTCAGAGGAAATAA (SEQ ID NO: 344)

30 **AOLFR187 sequences:**

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNLILI  
CVILSQAILHEPMYIFLSMLASADVLLSTTMPKALANLWLGYSHISFDGCLTQKFFIHFIFIHSA  
VLLAMAFDRYVAICSPRYVTILTSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIIAHTFCEH  
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLSQDARSKALSTCGSHICV  
35 ILLFYVPALFSVFA YRFGGRSIPCYVHILLASLYVVIPMLNPVIYGVRTKPILEGAKQMFSNLAK  
GSK (SEQ ID NO: 345)

ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG  
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA  
40 GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC  
AATGGCATCCTAATTTGTGTCATCCTCTCCAGGCAATCCTGCATGAGCCCATGTACATAT  
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG  
GCCAATTTGTGGCTAGGTTATAGCCACATTTCCTTTGATGGCTGCCTCAAAAAGTTCTT  
CATTCACTTCCCTCTTCATTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG  
45 CCATCTGCTCCCCCTGCGATATGTCAACATCCTCACAAGCAAGGTCATTGGGAAGATCGT  
CACTGCCACCCTGAGCCGAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC  
TGCACTATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA  
TCTGTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTTCTCTCCA  
CAGGCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC  
50 CTCCTTTCTCAAGATGCCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT  
CCTACTCTTCTATGTCCCTGCCCTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA  
TCCCATGCTATGTCCATATTCTCCTGGCCAGCCTCTACGTTGTCATTCTCCTATGCTCAAT  
CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA  
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

55

**AOLFR188 sequences:**

MFPSLPCVLLVQLPLMNENMQCFVFCSDSLLRMMVSRFIHVPFVKMKRIIVGGYSKHFFSN  
 ELLCVRPWSGKTWSIRHHIFDMELLTNLKFITDPFVCRLRHLSPTPSEEHMKNNVTEFILL  
 GLTQNPEGQKVLFVTFLLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK  
 5 MIVDLLSEKKTISFQGCMAQLFMDHLFAGA EVILLVMA YDRYMAICKPLHELITMNRRCVL  
 MLLAAWIGGFLHSLVQFLFIYQLPFCGNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC  
 AVTFFTILLSYGVILHSLKTSLEGKRKAFTYCASHVTVVILFFVPCIFLYARPNSTFPIDKSMTV  
 VLTFTPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

10 ATGTTCCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCCTTATGAATGAGAACAT  
 GCAGTGTTTTGTTTTCTGTTCTGTGATAGTTTGCTGAGAATGATGGTTTTCCCGCTTCATCC  
 ATGTCCTCATTTGTAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC  
 TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT  
 TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCTTTTGTGTGAGGC  
 15 TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAAATGTGACTG  
 AATTTATCCTCTTAGGGCTCACACAGAACCCTGAGGGGCAAAGGTTTTATTGTGCACATT  
 CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC  
 AGCCAGTCCCTGGGTTCCTCCCATGTACTTTTTCTGGCTTCTTATCATTATAGATACCGT  
 CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATT  
 20 CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTATTTGCTGGTGCTGAAGTCATT  
 CTTCTGGTGGTAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA  
 TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT  
 TCACTCATTGGTTCAATTTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG  
 ACAACTTCCTGTGTGATTTGTATCCCTTATTGAACTTGCTTGCACCAATACCTATGTCACT  
 25 GGGCTTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTCACCTTCTTCACTATCCTGC  
 TTTCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGAAGGGAAACGAAAAGC  
 TTTCTACACCTGTGCATCCACGTCAGTGTGGTCATTTTATTCTTTGTCCCCTGTATCTTCTT  
 GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA  
 TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT  
 30 GAGGAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA  
 (SEQ ID NO: 348)

**AOLFR189 sequences:**

MQQNNVPEFILLGLTQDPLRQKIVFVIFLYMGTVVGNMLIIVTIKSSRTLGSMPYFFLYLSF  
 35 ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDYVAICKPLRYP  
 TIMSQQVCHILIVLAWIGSLIHSTAQIILALRLPFCGPYLDHYCCDLQPLLKLACMDTYMINLLL  
 VNSGAICSSSFMIILISYIVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFIYTRPPTTFPMD  
 KMAVAFYTIGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

40 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA  
 GGCAGAAAATAGTGTTTGAATCTTCTAATTTTCTATATGGGAACTGTGGTGGGGAATAT  
 GCTCATTATTGTGACCATCAAGTCCAGCCGACACTAGGAAGCCCCATGTACTTCTTTCTA  
 TTTATTTTGTCTTTGCAGATTCTTGCTTTTCAACTTCCACAGCCCCATGATTAATTGTGGA  
 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA  
 45 CATTTATTTGGCTGCATGGAGATCTTTGTCTCATTCTCATGGCTGTTGATCGCTATGTGGC  
 CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT  
 GTTCTTGCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT  
 GCCTTTCTGTGGACCTATTTGATTGATCATTATTGCTGTGATTTGCAGCCCTTGTTGAAAC  
 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG  
 50 CTCAAGTAGTTTCATGATTTTGATAATTTTCATATATTGTCATCTTGCATTCACTGAGAAACC  
 ACAGTGCCAAAGGGAAGAAAAAGGCTCTCTCCGCTTGACAGTCTCACATAATTGTAGTCAT  
 CTTATTCTTTGGCCCATGTATATTCATATATACAGCCCCCGACCACTTTCCCATGGACA  
 AGATGGTGGCAGTATTTTATACTATTGGAACACCTTTCTCAATCCACTCATCTACACATCT  
 GAGGAATGCAGAAGTGAAAATGCCATGAGAAAG (SEQ ID NO: 350)

55

**AOLFR190 sequences:**

MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN  
 LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL  
 YAQTMPRRLCICLVLYSYTGGFVNAIILTSNTFTLDFCGDNVIDDFCDVPPLVKLACSVRESYQ  
 5 AVLHFLLASNVISPTVLILASYLSIITTLRIHSTQGRIKVFSTCSSHLISVTLYYGSILYNYSRPSSS  
 YSLKRDKMVSTFYTMLFPMNLNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGAAGTTCATCCTGCTGGGCTTCACCACAGATCCAG  
 GGATGCAACTGGGCCTCTTTGTGGTGTTCCTGGGTGTGTACTGTCTGACTGTGGTAGGAAG  
 10 TAGCACCTCATCGTGTTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTTGTCA  
 TTGGAAATCTGTCATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG  
 ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGTCAGTTCTTCTCTGC  
 CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC  
 ATCTCCAAGCCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT  
 15 ATATTCCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTACATTG  
 GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT  
 GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC  
 ATCTCCCCTACTGTGCTCATCCTTGCTCTTACCTCTCCATCATCACCACCATCCTGAGGAT  
 CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCACCTGATCTCCGTTA  
 20 CCTTATACTATGGCTCCATTCTCTACAACCTACTCCCGGCCAAGTCCAGCTACTCCCTCAAG  
 AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTCCCCATGTTGAATCCCATGATCTA  
 CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA  
 (SEQ ID NO: 352)

**AOLFR191 sequences:**

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS  
 FIDVCYISSTVPKMLSNLLQEQQTITFVGCHIQYFIFSTMGLSESLMTAMAYDRYAAICNPLLYS  
 SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQV  
 5 MTAILTMFFGLASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSIGIFVYLRSSS  
 GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTATCCTGCTGGGATTCTCAGATT  
 TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC  
 10 TGGAACCTCTCCCTCATTGTTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT  
 CTTCCTCAGTAACCTGTCCTTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC  
 TCTCCAACCTCTTACAGGAACAGCAAATATCACITTTTGTGGTTGTATTATTCAGTACTTT  
 ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT  
 ATGCTGCCATTTGTAACCCCTGCTCTATTTCATCCATCATGTCACCCACCCCTCTGTGTTGG  
 15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTGCT  
 TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACAITTTCTTCTGTGACATGCCCAACTGT  
 TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTT  
 TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA  
 TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC  
 20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT  
 CTTCAAGCTTTGACAGATTTGCATCTGTTTCTACACTGTGGTCATTCCCATGTTAAATCCC  
 TTGATTTACAGTTTGAGGAACAAAGAAATTAAGATGCCTTAAAGAGGTTGCAAAGAGA  
 AAGTGCTGCTGA (SEQ ID NO: 354)

**AOLFR192 sequences:**

MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYLITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV  
 DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRYAAALCKPLHY  
 TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCSRNVVEHFFCDAPLLTLSCSDNYISEM  
 VIFFVVGFNDFLSILVILISYLFIFITIMKMRSPGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS  
 30 HFMGTDKMASVFYAIVPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA  
 CTGCAGATCCCCTCTTCATAGTCTTCCCTTCATCTACCTCATCACTCTGGTTGGGAACCT  
 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCTCTCA  
 35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG  
 GTTCTCACAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATTCCTTCTTCTTG  
 TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC  
 ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC  
 ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATTCATACTGGGAACACTTTCAGGC  
 40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTCTGTGATGCTCCTCCTCTCTTGACT  
 CTCTCATGTTTCAGACAACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG  
 ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTATATTATACCATCATGAAG  
 ATGCGCTCACCTGAAGGACGCCAGAAGGCCITTTCTACTTGTGCTTCCCACCTTACTGCAG  
 TTTCCATCTTTTATGGGACAGGAATCTTATGTACTTACGACCTAACTCCAGCCATTTTCATG  
 45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG  
 TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAGACTGTAGGGAAGGCAA  
 AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

**AOLFR193 sequences:**

MENKTEVTQFILLGLTNDSELQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNPMYFFLSNLSLV  
 DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMA YDRYAAVCKPLHY  
 TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNEVHFFCDIPAVMVLSCSDRHISEL  
 VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIAVGIFYGTIIFMYLQPSSSH  
 SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:  
 55 357)

ATGGAAAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA  
 CTGCAGGTTCCCTCTTTATAACGTTCCCTTCATCTATATTATCACTCTGGTTGGAAACCT  
 GGGAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTTCTCA  
 GTAACCTGTCTCTAGTGGACTTTTGTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA  
 5 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT  
 AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA  
 GTGTGCAAAACCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA  
 TAGGCTCCTACCTCTGTGGTTTCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC  
 TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT  
 10 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTTCTTATTTATGTTGTGAGCTTCAATATCT  
 TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTTATCACCATCCTAAAGATG  
 CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTCATTGCAGTCGG  
 CATCTTCTATGGGACTATTATCTTCATGTAATTACAACCCAGCTCCAGTCACTCCATGGACA  
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCTCTGGTCTA  
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT  
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

#### AOLFR194 sequences:

MERQNSQSCVVEFILLGFSNYPELQGQLFVAFVLVIYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL  
 20 SVVDLSFSAVIMPEMLVVLSTKTTISFGGCF AQMYFILLFGGAECFLLGAMAYDRFAAICHPL  
 NYQMIMNKGVMKLIIFSWALGFM LGTVQTSWVSSFPFCGLNEINHISCETPAVLELACADTF  
 FEIYAFTGTFLIILVPFLLILLSYIRVLFALIKMPSTTGRQKAFSTCAHLTSVTLFYGTASMTY  
 LQPKSGYSPETKKVMSLSYSLTPLLNLIIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:  
 359)

25 ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC  
 CTGAGCTCCAGGGGCAGCTCTTTGTGGCTTTCTGGTTATTTATCTGGTGACCTGATAGG  
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT  
 TTCTCCTGAACTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT  
 30 GGTGGTCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT  
 TTCATCCTTCTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT  
 TGCTGCAATTTGCCATCCTCTCACTACCAAATGATTATGAATAAAGGAGTTTTTATGAAA  
 TTAATTATATTTTCTATGGGCCTTAGGTTTATGTTAGGTACTGTTCAAACATCATGGGTATC  
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT  
 35 TAGAAGTTGCATGTGCAGACACGTTTTTGTGAAATCTATGCATTACAGGCACCTTTTTG  
 ATTATTTTGGTTCCCTTCTTGTGATACTCTTGTCTTACATTGAGTTCTGTTGCCATCCTG  
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTCCACCTGTGCCGCTCACCTCACAT  
 CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC  
 ACCGGAACCAAGAAAGTGATGTCATTGTCTTACTCACTTCTGACACCACTGCTGAATCTG  
 40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG  
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

#### AOLFR195 sequences:

MIVQLICTVCFLAVNTFHVRSFDFLKADDMGEINQTLVSEFLLGLSGYPKIEIVYFALILVMY  
 45 LVILIGNGVLIASIFDSHFHTPMYFFLGNL SFLDICYTSSSV PSTLVSLISKRNISFSGCAVQMF  
 GFAMGSTECLLLGMMAFDRYVAICNPLRYPIILSKVAYVLMASVSWLSGGINS AVQTLLAMRL  
 PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVPLMVIFFSYMFILYTIQMNSATG  
 RRKAFTSCSAHLTVVIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSLR  
 NKDVKA AVKYLLNKPIH (SEQ ID NO: 361)

50 ATGATTGTTCAAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC  
 TTCTTTTGATTTCCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTTGTGTCAGAA  
 TTTCTTCTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT  
 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT  
 55 CTCATTTTCACACACCAATGTACTTCTTCTGGGCAACCTCTCTTTCTGGATATCTGCTAT  
 ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCTT



TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT  
 TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC  
 ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGAATAA  
 ATTCAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA  
 5 TCATTTTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA  
 TTATCACCATGGTGATATCAAATATGGCCTTCCTGGTTCTTCCACTGATGGTCATTTTTTC  
 TCCTATATGTTTCATCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG  
 CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTACGGTACCATCTTCTTT  
 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC  
 10 AAGCTCATTTCTCTGTTTTATGGGGTAGTGACCCCATGCTGAATCCTATACTCTATAGCTT  
 GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAACCAATTCACTA  
 A (SEQ ID NO: 362)

**AOLFR196 sequences:**

15 MLESNYTMPTEFLVFGFTDYPLRVTLFLVLLVYTLTMVGNILLIILVNINSSLQIPMYFSLNL  
 SFLDISCSTAITPKMLANFLASRKSSIPYGCALQMFFAFADAECILILAAAMAYDRYAAICNPLL  
 YTTLMSSRRVCVCFIVLAYFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPPLLALSCTDTQINQL  
 LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS  
 20 YSLDTDKVVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ  
 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC  
 TACCTCTCAGAGTCACACTGTTCTTGGTATTCCTTCTGGTATATACATTAAGTATGGTCGGA  
 AATATACTCTTAATAATTCTAGTTAATATTAATCAAGCCTTCAAATCCCATGTATTATTT  
 25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTCTTACAGCAATCACTCCTAAATGCTGG  
 CAAACTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT  
 CTTGCTTCTTTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG  
 CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT  
 CATTGTGTTGGCATATTTCACTGGAAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC  
 30 AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCACCTCTTCT  
 GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA  
 TCCAGACCAGCACTTTTGTGGTAATATTTATTTCTTACTTCTGCATCCTCATCACTGTGTTG  
 AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCACCTCATAG  
 CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCACTAGCTATTCC  
 35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA  
 TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA  
 TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAAGAATAGTCAATATCTAA (SEQ ID NO:  
 364)

**AOLFR197 sequences:**

40 MCYLSQLCLSLGEHTLHMGMVRHTNESNLAGFILLGFSDDYPQLQKVLFLILILYLLTILGNTTI  
 ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS  
 TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCMALASMAWLSGIATTLVQSTLTLLQLPFCGH  
 RQVDHFICEVPVLIKACVGTTFNEAEELFVASILFIVPVSFILVSSGYIAHAVLRIKSATRRQKAF  
 45 GTCFSLTLTVTIFYGTIIFMYLQPAKSRSDQGKFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK  
 VLAKALGVNII (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG  
 TGAGACATAACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTCTGATTATCC  
 50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTGGGGA  
 ATACCACCATCATTCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC  
 CTTTCTCATCTCTCTTCTGTACCGCTGCTTCACCAGCAGTGTTATCCCCAGCTCCTGGT  
 AAACCTGTGGGAACCCATGAAAACATCGCCTATGGTGGCTGTTTGGTTACCTTTACAAC  
 TCCCATGCCCTGGGATCCACTGAGTGCGTCTCTTGGCTCTGATGCTGTGACCGCTATGT  
 55 GGCTGTCTGCCGTCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG  
 CATCTATGGCATGGCTCAGTGGAATAGCCACCACCCTGGTACAGTCCACCCTCACCCTGCA



GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC  
AAGCTGGCTTGTGTGGGCACACGTTTAAACGAGGCTGAGCTTTTTGTGGCTAGTATCCTTT  
TCTTATAGTGCCTGTCTCATTTCATCCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTG  
AGGATTAAAGTCAGCTACCAGGAGACAGAAAGCATTCGGGACCTGCTTCTCCACCTGACA  
5 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT  
CCAGGGACCAGGGCAAGTTTGTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC  
TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA  
GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPQLPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL  
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMAFYDRYAAVCKP  
LHYTTMTASVGACLAALGSYVCGFLNLSFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH  
TSEVILVMSSFNIFVLLVIFISYLFIFITILKMHSAGHQAALSTCASHFTAVSVFYGTVIFYLQ  
15 PSSSHSMDTDKMASVFYAMIHPMLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC  
TACAGATCCCCCTCTTTATCTTGTTACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG  
GGGATGATGTTGCTGATCCTGATGGACTCTGTCTCCACACCCCATGTACTTTTCTCCTCAG  
20 TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG  
TTCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTTCTGATGTTCTTCTTGT  
AGCCTTGCCACGGTGGAAAATTACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA  
GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC  
TAGGCTCATATGTCTGTGGCTTCTTAAATGCCTCATTCCACATTGGGGGCATATTCAGTCTC  
25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTTCTGTGATGTTCCAGCAGTCATGGCTCT  
GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT  
TTTTGTCTTCTAGTTATCTTTATCTCCTACTTGTTTCATATTCATCACCATCTTGAAGATGC  
ATTCAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC  
CGTCTTCTATGGGACAGTAATCTTCATCTACTTGACGCCAGCTCCAGCCACTCCATGGAC  
30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCATGCTGAACCCTGTGGTCT  
ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCAAAAAT  
TTCTATAA (SEQ ID NO: 368)

**AOLFR199 sequences:**

MDTGNTLPQDFLLGFPGSQTQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS  
NLSFLEIWYTTAAVPKALAILLGRSQTISFTSCLLQMYFVFLGCTEYFLLAAMAYDRCLAICYP  
LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFFCDIAPWIALACTNTQA  
VELVAFVIAVVILSSCLITFVSYVYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR  
TSIKDALDLIAVHVLNTVVPVLPNPFYTLRNKEVRETLKKWKWK (SEQ ID NO: 369)

ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC  
AAACTCTTCAGCTCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT  
AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCATGTACTTCTT  
45 TCTGAGCAACCTCTCCTTCTGGAGATTTGGTATACCACAGCAGCAGTGCCCAAAGCACTG  
GCCATCCTACTGGGGAGAAGTCAGACCATATCATTTACAAGCTGTCTTTTGCAGATGTACT  
TTGTTTTCTCATTAGGCTGCACAGAGTACTTCTCCTGGCAGCCATGGCTTATGACCGCTGT  
CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC  
TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCACAGCCCTCATCAG  
TGGCCTGTCTTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA  
50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT  
GGTTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATCC  
TCAGGATCCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC  
CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCTTCCACGTCCGCACCTCTATCAAAGAT  
GCCTTGGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTAAACC  
55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG  
GAAAATAA (SEQ ID NO: 370)

**AOLFR200 sequences:**

MTRKNYTSLTEFVLLGLADTLELQIILFLFLVIYTLTVLGNLGMILLIRIDSQ LHTPMYFFLANL  
 SFVDVCNSTTITPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL  
 5 YSLMSRTVYVKMAAGAFAGLLNFMVNTSHVSSLSFCDSNVIIHFFCDSPPLFKLSCSDTILKE  
 SISSILAGVNIVGTLLVILSSYSYVLFISFMSHSGEGRHRAFSTCASHLTAILFYATCIYTYLRPSS  
 SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC  
 10 TGGAGCTACAGATTATCCTCTTTTTGTTTTTCTTGATTTATACACTTACAGTACTGGGA  
 AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCAGCTTCACACACCCCATGTATTTCTT  
 CCTGGCTAACCTGTCCTTTGTGGACGTTTGTAACCTCACTACCCCAAAGATGCTG  
 GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTGCTGGCTGCTTCTACAGATGTA  
 TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTTAATGGCCTATGACAGGTA  
 15 TGC GGCCATATGTCGCGCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA  
 ATGGCAGCCGGGGCTTTTGTGTCAGGGTTGCTGAACTTCATGGTCAACACAAGCCATGTCA  
 GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT  
 TTCAAGCTCTCTTGTTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG  
 TGAATATTGTGGGGACTCTGCTTGTCATCCTCTCCTCCTACTCCTACGTTCTCTCTCCATT  
 20 TTTTCTATGCATTGCGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCTCTCACCTGA  
 CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCCAGCTAC  
 TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC  
 CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCITTAGCGAATGTAATTAGCA  
 GGAAAAGGACCTCTTCCTTTCTGTGA (SEQ ID NO: 372)

25

**AOLFR201 sequences:**

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL  
 SFLDICYTTTSPSTLVSFLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMMAFDYVAICNPLR  
 YPIIMSKDAYVPMAGSWIIGAVNSAVQSVFVQLPFCRNNIINHFTCEILAVMKLACADISDN  
 30 EFIMLVATTLFILPPLLIIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS  
 KETLNSDDL DATDKIISMFGVMTMPMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:  
 373)

ATGGAATGGGAAAACCACACCATTTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC  
 35 CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG  
 AATGGTACTCTCATTTTAATCAGCATCTTGGACCTCACCTTCACACCCCTATGTACTTCTT  
 TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG  
 TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGACGTGCAGATGTTTCT  
 CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT  
 40 GTGGCTATCTGCAACCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA  
 TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTTTGTGGT  
 ACAATTGCCCTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTGGCTGTC  
 ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT  
 TGTTCATATTGACACCTTTGTTAATTAATCATGTCTCTTACACGTTAATCATTGTGAGCATC  
 45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCTCTACCTGTTACGCCCATCTGA  
 CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA  
 GACACTTAATTTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG  
 ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA  
 GTAAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

50

**AOLFR202 sequences:**

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL  
 SFLDICYTTTSPSTLVSFLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDYVAICNPLR  
 YPIIMSKDAYVPMAGSWIIGAVNSAVQTVFVQLPFCRNNIINHFTCEILAVMKLACADISGN  
 55 EFILLVTTTLFLLPPLLIIIVSYTLIISIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDATDKLIFIFYRVMTPMMNPLIYSLRNKDVKEAVKHLLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCATTCTGGTGGAAATTTTTCTGAAGGGACTTTCTGGTCACC  
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG  
AATGGTACTCTCATTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT  
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG  
TGAGCTTCCTTTT CAGAAAGAAAGACCATTTCCTTTCTGGCTGTGCAGTGCAGATGTTCTT  
10 CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT  
GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA  
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTGTTGTGGT  
ACAATTGCCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTTCTAGCTGTC  
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT  
TGTTCTTATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC  
15 TTCAAAATTAGCTCTTCGGAGGGGAGAAGCAAACCTTCTCTACCTGCTCAGCTCGTCTGA  
CTGTGGTGATAACATTCTGTGGGACCATCTTCTCATGTACATGAAGCCCAAGTCTCAAGA  
GACACTTAATTCAGATGACTTGGATGCCACTGACAACTTATATTATATTCTACAGGGTG  
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA  
GTAAACACCTACTGAGAAGAAAAAATTTTAACAAGTAA (SEQ ID NO: 376)

20

**AOLFR203 sequences:**

MRKQNQSCVVEFILLGFSNFPQLVQLFGVFLVIYVVTLMGNAIITVIISLNQSLHVP MYLFLLN  
LSVVEVSFSAVITPEMLVVLSTEKT MISFVGCAQMYFILLFGGTECFLLGAMAYDRFAAICHPL  
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLCETPPVLELVCA DTF LF  
25 EIYAFTGTILIVMVPFLLILLSYIRVLFAILKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ  
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRTLKLRWKVILHTF (SEQ ID NO: 377)

ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC  
30 CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCTAGTTATTTATGTGGTGACCCTGATGGG  
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT  
TCTCCTGAACCTATCTGTGGTGGAGGTGAGTTT CAGTGCAGTCATTACGCCTGAAATGCT  
GGTGGTGCTCTCTACTGAGAAAATATGATTTCTTTTGTGGGCTGTTTTGCACAGATGTAT  
TTCATCCTTCTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT  
TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTTATGAAA  
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT  
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCCGTA  
CTAGAGCTTGTGTGTGCAGACACCTTCTATTGAAATCTATGCCTTCACAGGCACCAATTT  
GATTGTTATGGTTCCTTCTTGTGATCCTCTTGTCTTACATTGAGTTCTGTTTGCCATCCT  
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCCTTTTCCACCTGTGCCTCTCACCTCACA  
40 TCTGTGACCCTGTTCTATGGCACAGCCAATGACCTATTACAAACCAATGACCTCACTC  
ACCCGAAACCAAGAAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG  
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAACTATGGCGAAGA  
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

45

**AOLFR204 sequences:**

MEKKKNVTEFILIGLTQNPIMEKVTFVVLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL  
IDTVYSSSSAPKLIVDSFQEKIISFNGCMAQAYA EHIFGATEILLTVMACDCYVAICKPLNYTT  
IMSHSLCILLVAVAVVGGFLHATIQILFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV  
AVNSGFICLLNFLILVVSYVILRSLKNSLEGRCKALSTCISHIIVVLFVPCIFVYLRSVTTLP I  
50 DKAVAVFYTMVVPMLNPVYTLR NAEVKS AIRKLWRKKVTS DND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCAT A  
ATGGAGAAAGTCACGTTTGTAGTATTTTGGTCTTTACATGATAACACTTT CAGGCAACC  
TGCTCATTGTGGTTACCATTACCACCAGCCAGGCTCTGAGCTCCCCCATGTACTTCTCCTG  
55 ACCCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTT CAGCTCCTAAGTTGATTGTGGA  
TTCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

CACATTTTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG  
 CCATCTGCAAACCTCTGAACTACACAACCATATGAGCCACAGCCTGTGCATTCTCCTGGT  
 GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTCAGATTCTCTTTACAGTATGG  
 CTGCCCTTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTTAAA  
 5 ACTTGTGTCATAGACACTCATACCCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT  
 GCTTATTAACCTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC  
 AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCACATCATAGTAGTTG  
 TCTTATTCTTTGTGCCCTGTATATTTGTGTATCTGCGCTCAGTGACCACTCTGCCATTGAT  
 10 AAAGCTGTTGCTGTATTTTATACTATGGTGGTCCCAATGTAAATCCCGTGGTCTACACAC  
 TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAAGTGACTTCAG  
 ATAATGATTAA (SEQ ID NO: 380)

#### AOLFR205 sequences:

MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFIILPGNFLIIFTIKSDPGLTAPLYFFLGNLAFL  
 15 DASYSFTVAPRMLVDFLSAKKIISYRGCTQLFFLHFLGGGEGLLLVMAFDRIYAIICRPLHYPT  
 VMNPRTCYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVPQVIKLACTDTFVVEL  
 LMFVNSGLMTLLCFLGLLASVAVILCRJRGSSSEAKNKAMSTCIHIIVIFMFGPGIFIYTRPFRA  
 FPADKVVSLFHTVIFPLLPVITYTLRNQEVKASMKKVFNKHIA (SEQ ID NO: 381)

20 ATGGAAAGCGAGAACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT  
 CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTAAATATTCTACTTCATCATCCTCCCTGG  
 AAATTTTCTCATTATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCT  
 TTCTGGGCAACTTGGCCTTCCTGGATGCATCCTACTCCTTCACTGTGGCTCCCCGGATGTTG  
 GTGGACTTCCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT  
 25 TCTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTA  
 CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTCATGAACCCTAGAACCTGCTATGCA  
 ATGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCCCTCATCCT  
 CCGCTTGCCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCACAGGTC  
 ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC  
 30 TGATGACACTCCTGTGCTTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTGTGCGATA  
 CGAGGGTCTTCTTCTGAGGCAAAAAACAAGCCATGTCCACGTGCATCACCCATATCATTG  
 TTATATTCTTCATGTTTGGACCTGGCATCTTCATCTACACGCGCCCTTACAGGGCTTTCCCA  
 GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTTCTTTGTTGAATCCTGTCAATTA  
 TACCTTCGCAACCAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTTAATAAGCACATAGC  
 35 CTGA (SEQ ID NO: 382)

#### AOLFR206 sequences:

MANRRNVTEFILLGLTENPKMQKIIFVVSIVYINAMIGNVLIVVTITASPSLRSPMYFFLAYLSFI  
 40 DACYSSVNTPKLITDSLYENKTILFNGCMTQVFGEHFFRGVEVILLTVMAYDHYVAICKPLHYT  
 TIMKQHVCSSLVGVSWVGFLHATIQILFICQLPFCGPNVIDHFMCDLYTLINLACTNTHTLGLF  
 IAANSFGICLLNCLLLLVS CVVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCIFVYMRPPATL  
 PIDKAVAVFYTMITSMLNPLIYTLRNAQMKNAIRKLCRKAISSVK (SEQ ID NO: 383)

45 ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA  
 ATGCAGAAAATCATATTTGTTGTGTTTTCTGTCTATCTACATCAACGCCATGATAGGAAATG  
 TGCTCATTGTGGTCACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTAATTTTCTCCTG  
 GCCTATCTCTCCTTATTGATGCCTGCTATTCTCTGTCAATACCCCTAAGCTGATCACAGA  
 TTCCTCTATGAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA  
 50 CATTTTTTTCAGAGGTGTTGAGGTCATCCTACTTACTGTAATGGCCTATGACCACTATGTGG  
 CCATCTGCAAGCCCTTGCCTATACCACCATCATGAAGCAGCATGTTTGTAGCCTGCTAGT  
 GGGAGTGTGATGGGTAGGAGGCTTTCTTCATGCAACCATAACAGATCCTCTTCATCTGTCAA  
 TTACCTTTCTGTGGTCTTAATGTGATGATCACTTTATGTGTGATCTCTACACTTTGATCAA  
 TCTTGCCCTGCACTAATACCCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTCATAT  
 55 GCCTGTTAACTGTCTCTTGCTCCTGGTCTCCTGCGTGGTCATACTGTACTCCTTAAAGACC  
 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCTACCTGTGTCTCCACATCACAGTTGTCA  
 TCTTATCCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTAAACCCCTTAATCTACACCTT  
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG  
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDSHLHTPMYFFLCN  
LSFLDVCYTSSSVPLILASFLAVKKVVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICY  
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAAMQLPFCANNVIKHFVCEILAILKLACADI  
SINVISMTGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIFYGTIFFMYAKP  
10 ESKASVDSGNEDIEALISLFYGVMTPLNPLIYSLRNKDVKAAVKNILCRKNFSDGK (SEQ ID  
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTTCTGGTAGGGCTTTCTGCCACC  
CAAAGCTCCAGACAGTTTTCTTCGTTCTAATTTGTGGATGTACCTGATGATCCTGCTTGGA  
15 AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCCATGATTTCTT  
CCTCTGTAATCTTTCTTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATTCTTG  
CCAGCTTTCTGGCAGTAAAGAAAAAGTTTCTTCTCTGGGTGTATGGTGCAAATGTTTAT  
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT  
GTGGCCATCTGCTACCCACTGAGATAACCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA  
20 TGGCAGCTGGGTCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT  
GCAGTTACCAATTCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTCTGGCTATCT  
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTCGAATCTGAT  
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT  
GAGGATTCCTTCCACTGAAGGAAAAACATAAGGCCTTCTCCACCTGCTCAGCCCACCTGACA  
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT  
CTGTTGATTCAAGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT  
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC  
AAAAACATACTGTGTAGGAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL  
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP  
LRYPVIMNRRTCQIAAGSWMTGCLTAMVEMMSVLPISLCGNSIINHFTCEILAILKLVCVDT  
LVQLIMLVISVLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFGTALSMH  
35 LKPSAVDSQEIDKFMAVYAGQTPMLNPITYSLRNKEVKVALKKLLIRNHFNTAFISILK (SEQ  
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCCTGGGATTTTTTCACTACCC  
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC  
40 AACATTTTTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT  
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG  
CAAACCTTTGTTTCAGGGAGAAACACTATTTCAATTCTCAGGGTGCGCCACTCAGATGTACCT  
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCATGATGGCATATGACCGGTAT  
GTGGCCATCTGCAACCCCTGAGATAACCTGTCATCATGAATAGGAGAACCTGTGTGCAGA  
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAATGATGTCTGTGCT  
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTCACTTGTGAAATTCTGGCCATCT  
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT  
TCTTCTCCCATGCCAATGCTACTCATTGTATCTTATGCATTTATCCTCGCCAGTATCC  
TGAGAATCAGCTCAGTGGAAGGTGGAAGTAAAGCCTTTTCAACGTGCACAGCCCACCTGA  
50 TGGTGGTAGTTTTGTTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA  
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT  
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA  
GAAATCATTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

**AOLFR209 sequences:**

MDKINQTFVREFILLGLSGYPKLEIFFALILVMYVVILIGNGVLIASILDSRLHMPMYFFLGNLS  
 FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLGMMAFDTRYVAICNPLRY  
 5 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV  
 TLAVSNIAFLVPLLVIFFSYMFILYTLRTNSATGRHKAFSTCSAHLTVVIIFYGTIFFMYAKPKS  
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:  
 389)

10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC  
 CCAAACCTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC  
 AATGGTGTTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT  
 CCTGGGCAACCTCTCTTCTGGAATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG  
 TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCAGATGTTCTT  
 15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCCTCCTTGGCATGATGGCATTTGATCGTTAT  
 GTGGCCATCTGTAACCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC  
 TGACTTCTGTATCATGGCTTTCTGGTGGAAATCAATTCAACTGTGCAAAACATCACTTGCCAT  
 GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTCTTATGCGAGATCTTAGCTGTCC  
 TAAAATTAGCTTGTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT  
 20 TTCCTAGTTCTTCTGCTCGTGATTTTCTCTCTATATGTTTCATCCTCTACACCATCTTG  
 CGAACGAACTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG  
 TGGTGATCATATTTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCCAGGACCTC  
 CTTGGGAAAGACAACCTTGCAAGCTACAGAGGGGCTTGTTCATGTTTTATGGGGTTGTGA  
 CCCCCATGTTAAACCCATAATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA  
 25 ATATTTGCTGAGCAGGAAAGCTATTAACCAGTAA (SEQ ID NO: 390)

**AOLFR210 sequences:**

MMGRRNDTNVADFILTLGLSDSEEVQMALFMLFLLIYLITMLGNVGMILLIIRLDLQLHTPMYFFL  
 THLSFIDLSYSTVVPKTLANLLTSNYISFTGCAQMF CFVFLGTAECYLLSSMAYDRYAAICSP  
 30 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVSMSRLHFCDNSNIHHFFCDTSPILALSCTD TDN  
 TEMLIFIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTFYGTMIFTYLPK  
 RKSYSLGRDQVAPVFYTIVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC  
 35 TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT  
 GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT  
 TTTTCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAC  
 CTTAGCGAACTTACTGACTTCCAATAATTTCTTACGGGCTGCTTTGCCAGATGTTCT  
 GTTTTGTCTTCTTGGGTACTGCTGAATGTTATCTTCTCTCCTCAATGGCCTATGATCGCTAT  
 40 GCAGCGATCTGCAGTCTCTACACTACACAGTTATTATGCCAAAAGGCTCTGCCTCGCTC  
 TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC  
 AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACACTTCCCCAATTTT  
 AGCTCTGTCTGCACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTCC  
 ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT  
 45 GAAAATTAATCCACTTCAGGAAAGCAGAAAGCTTCTCTACTTGCGTCTCTCATCTCTTG  
 GGAGTCACCATCTTCTATGGAACATGATTTTACTTACTTAAAGCCAAGAAAGTCTTATT  
 CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC  
 ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG  
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

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**AOLFR211 sequences:**

MMGRRNNTNVADFILMGLTLSEEIQMALFMLFLLIYLITMLGNVGMILLIIRLDLQLHTPMYFFL  
 THLSFIDLSYSTVVPKTLANLLTSNYISFTGCAQMF FFAFLGTAECYLLSSMAHDRYAAICSP  
 LHYTVIMSKRLCLALITGPYVIGFIDSFVNVSMSRLHFYDSNVIHHFFCDTSPILALSCTD TYNT  
 55 EILIFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTFYSTLIFTYLPKPK  
 SYSLSLGRDQVASVFYTIVIPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT  
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG  
 GGGAAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT  
 5 TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAACC  
 TTAGCGAACTTACTGACTTCCAACATATTTCTTTACGGGCTGCTTTGCCAGATGTTCTT  
 TTTTGCCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCAGATGCTGCTATG  
 CAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT  
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA  
 10 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTCTGTGACACTTCCCCAATTTTA  
 GCTCTGTCTGCTGACTGATACATAACACCGAAATCCTGATATTCATTATTGTTGGTTCCAC  
 CCTGATGGTGTCCCTTTTACAATATCTGCATCCTATGTGTTCACTTCTTTTACCATCCTGA  
 AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCCTCTCTCATCTCTTGGG  
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCCT  
 15 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGCTGAATCCACT  
 CATTTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTGCATCAGAGTCATGCAGAGAAG  
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

#### AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPQLVSLFLMFLFYLFVTLGNLGLITLIRMDSQLHTPMYFFLSN  
 LAFIDIFYSSVTVPKALVNFQSNRRSISFVGVQMYFFVGLVCCECFLLGSMAYNRYIAICNPL  
 LYSVVMSSQKVSNNWLGVMPPYVIGFTSSLSVWVISSLAFCDSINHHFCDTTALLALSCVDTFGT  
 EMVSFVLGFTLLSSLLIITVTYIIIIISAILRIQSAAGRQKAFSTCASHLMVAVTIFYGSLIFTYLPD  
 NTSSLTQAQVASVFYTVIPMLNPLIYSLRNKDVKNALLRVIHRKLP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTGCAAATCACC  
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATTCAGTGTTTTGGGA  
 AACCTGGGACTGATCAGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT  
 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG  
 30 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAAATGTACTT  
 TTTTGTGGATTGGTGTGTTGTGAGTGTTCCTTCTGGGATCAATGGCCTACAATCGCTACA  
 TAGCAATCTGCAATCCCTTACTGTATTGAGTAGTCATGTCCCAAAAAGTGTCCAATGGCT  
 GGGAGTAATGCCATATGTGATAGGCTTCACAAGCTCGCTGATATCTGTCTGGGTGATAAGC  
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTTGTGACACCACAGCTCTTTTAGC  
 35 ACTCTCCTGTGTAGATACATTGGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT  
 CTTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCTCAGCCATCCTGAG  
 GATCCAGTCAGCAGCAGGCAGGCAGAAAGGCCTTCTCCACCTGCGCATCCACCTCATGGCT  
 GTAACATCTTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT  
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCAATCCCATGCTGAATCCACTC  
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA  
 CTTTTCCATGA (SEQ ID NO: 396)

#### AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSHPRL  
 EAVLFVFLFFYLLTLVGNFTIIISYLDPPPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK  
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA  
 SSLIHATFTLQLPLCGNHRDLHFICEVPALLKLACVDTTVNELVLFVSVLFFVIPPALISISYGF  
 TQAVLRIKSVEARHKAFSTCSSHLTVVIFYGTHIYVYLQPSDSYAQDQGKFISLFYTMVPTLNP  
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA  
 ATTTAATTGTTTGGATGTACCCATTCCATTCTGCCTTAGGTGCGGATCCCCCTGGAGGG  
 ATGGGATTGGGCAATGAGAGTTCCTAATGGATTTATCCTTCTAGGCTTCTCAGACCACC  
 CTCGTCTGGAGGCTGTTCTCTTTGTATTTGTCTTTTCTTCTACCTCCTGACCCTTGTGGGA  
 55 AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTCTCATACCCCAATGTACTTTT  
 TCTCAGCAACCTCTCTTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG



TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT  
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC  
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC  
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTCCCTAATCCATGCAACTTTTACCTTG  
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT  
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGCTTTTGTGTAGTGTCTGT  
 TTGTTGTCATTCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG  
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCACCTTACAG  
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC  
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT  
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAACTTCTCTCGGGA  
 AAATTGTGA (SEQ ID NO: 398)

**AOLFR214 sequences:**

15 MDKSNSSVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN  
 LSFVDICQASFATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY  
 YVVMISRRCTCTVLMISWAVSLVHTLSQLSFTVNLFPFCGPNVVDSEFFCDLPRVTKLACLDSEYIE  
 ILIVNSGILSLSTFSLLVSSYIILVTWVKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS  
 PLDKFLAIFYTVFTPVLNPIIYTLNRNMDKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID  
 20 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTAAGTGTGGGACTCTGTAGTTCTC  
 AAAAACTCCAGCTTTTCTATTTTGTCTTCTCTGTGTTGTATACAGTCATTGTGCTGGGA  
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT  
 25 CTGCGGAAACCTTTCTTTGTTGACATTTGTCAGGCTTCTTTGCTACCCCTAAATGATTG  
 CAGATTTTCTGAGTGACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTCTTT  
 ATTCACCTTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCCTATGACAGGTATG  
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT  
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGACACATTAAGCCAGTTATCATTACTGTG  
 30 AACCTGCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTTGTGATCTTCTCGAGTCAC  
 CAAACTTGCCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAATT  
 CTTTCCCTAAGCACTTCTCTCTCTGGTCAGCTCCTACATCATTATTCTTGTACAGTTTG  
 GCTCAAGTCTTCAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGCAGTA  
 GTAATATTATTCTTTGGACCTTGCATCTTCATCTATGTGTGGCCCTTTACCATCTCTCCTTT  
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTTACCCCCGTCCTAAACCCCATTTTATA  
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC  
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:  
 400)

**AOLFR215 sequences:**

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNSPMYFLLSNL  
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH  
 YSTIMNRRLCVFVSISWAVGLHSVSHLAFTVDLPFCGPNEVDSEFFCDLPLVIELACMDTYEM  
 EIMTLTNSGLISLSCFLALIISYTHLIGVRCRSSSGSSKALSTLTAHITVVLFFGPCIFYIWPFSRL  
 45 PVDKFLSVFYTVCTPLLNPIIYSLRNEDVKAAMWKLNRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT  
 GGGGACTTCAACTTTTCTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC  
 AATGTCTTAATTATTGTCAATTATTTCTTTTGAAGTCTCCTATGTACTTCTTG  
 50 CTCAGTAATCTTTCTTTCAATTGATATCTGTGAGTCTAAGTCTTGGCAGGCTGATGCTTGT  
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCCAAGATGCTTGT  
 CTTACAGTTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA  
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT  
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCATTCTGTGAGCCACTTGGCTTTTACAGTGG  
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA  
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG



ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG  
 ATGCAGGTCCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAAGTCCCACATCACAGTG  
 GTCATTCTTTTCTTCGGGCCCTTGCAATTTATTTCTATATATGGCCTTTAGCAGACTTCCTGT  
 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTGAACCCCATCATCTACT  
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT  
 CCTGGAAAACTAG (SEQ ID NO: 402)

**AOLFR216 sequences:**

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNLIVITVIVDPHLHSPMYFLL  
 10 TNLSIIDMSLASFATPKMITDYLGHKTIISFDGCLTQIFFLHLFTGTEIILLMAMSFDRYIAICKPL  
 HYASVISPPQVCVALVVASWIMGMHSMQVIFALTLPCGPPYEVDSSFFCDLPVVFQLACVDY  
 VLGLFMISTSGIHALSCFIVLFNSYVIVLVTVKHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW  
 PLSSFLTDKILSVFYTIPTLNPITYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAAATTTGTTTTGCTGGGGCTCTCTAATTCCT  
 GGGAACTACAGATGTTTTCTTTATGGTGTTTTCAATGCTTTATGTGGCAACAATGGTGGG  
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC  
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTTTCGCCACCCCAAAGATGATT  
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTGATGGCTGCCTTACCCAGATATTCT  
 20 TTCTCCACCTTTTCACTGGAAGTGAAGTCATCTTACTCATGGCCATGTCCTTTGATAGGTAT  
 ATTGCAATATGCAAGCCCCTGCACTATGCTTCTGTCTATTAGTCCCCAGGTGTGTGTTGCTCT  
 CGTGGTGGCTTCCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC  
 ACGTTACCATCTGTGGTCCCTATGAGGTAGACAGCTTTTTCTGTGACCTTCCTGTGGTGTT  
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCCTCTTATGATCTCAACAAGTGGCATA  
 25 ATTGCGTTGTCTGTTTTATTGTTTTATTTAATTCATATGTTATTGTCTGTTACTGTGAA  
 GCATCATTCTTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTCTATTGTG  
 TCTTCTGTTCTTTGGGCCATGCATCTTCATCATGTGGCCACTAAGCAGCTTTCTCACA  
 GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC  
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAACTGAAAAATAGGTTTCTAAATTT  
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

**AOLFR217 sequences:**

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH  
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKASIFEGCMTQMFFLHLLGGAEIVLLISMSFD  
 35 RYVAICKPLHYLTIMSRMCVGLVILSWIVGIFHALSQLAFTVNLPCGPNVDSFFCDLPVVIK  
 LACVDYILGVFMISTSGMIALVCFILLVISYTIILVTVRQRSSGGSSKALSTCSAHFTVVTLLFFGP  
 CTFIYVWPFTNFPIDKVLVSFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP  
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC  
 GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTTT  
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTCATCA  
 GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC  
 CCTGGCCTCATTTGCCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC  
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGCTGAGATTG  
 TACTGCTGATCTCCATGTCCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA  
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTTCTGGATTGTGCGGCATCT  
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT  
 AGACAGTTTCTTTGTGACCTCCCTTTGGTGATTAACTTGCTTGTGTCGACACATATATTC  
 50 TGGGGGTGTTTCATGATCTCAACCAAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT  
 GATCTCTTACACTATCATCCTGGTCACCGTTCGGCAGCGTTCCTCTGGTGGATCCTCCAAA  
 GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCCCTTTCTTTGGCCCATGCACTTT  
 CATTTATGTGTGGCCTTTCACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA  
 TATACTCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC  
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA  
 (SEQ ID NO: 406)

**AOLFR218 sequences:**

METANYTKVTEFVLTGLSQTREVQLVLFVIFLSFYLFILPGNIICTIRLDPHLTSPMYFLLANLA  
 LLDIYWSSITAPKMLIDFFVERKIIISFGGCLAQFLHFVGAEMFLLIVMAYDRYAAICRPLHYA  
 5 TIMNRRLLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRACANTFPEELVM  
 ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVVLMFGPSIYIYARFDF  
 SFSLDKVVSVFHTVIFPLLNPIHYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC  
 10 GGGAGGTCCAAGTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA  
 AATATCCTTATCATTTGCACCATCAGGCTAGACCCCTCATCTGACTTCTCCTATGTATTTCTT  
 GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTCCATTACAGCCCCTAAAAATGCTCA  
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT  
 CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT  
 15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGCTCTGCTGTATCCT  
 GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCACTTCTATAATACAGGTGGCTCTCATTGTT  
 CGACTTCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTG  
 TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT  
 GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCTATGCCTTCTTCTGGCCTTGCTCA  
 20 AGAAACATTCAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTTCCACAT  
 TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT  
 TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATTCCTTTACTTAATCCCAT  
 ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT  
 ATTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

25

**AOLFR219 sequences:**

MLTSLTDLCSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNF  
 LILTVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS  
 EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWVFGFIHTTSQLAFTVNLFP CGPN  
 30 KVDSFFCDLPLVTKLACIDTYVVSLIVADSGFLSLSSFLLLVSYTVILVTVNRSSASMAKAR  
 STLTAHITVVTLFFGPCIFIYVWPFSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSKLKS  
 RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAAGTATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT  
 35 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG  
 TCTAGTTCAAGGGAGCTCCAACCTTTCTTGTTCCTTACATTTTCACTACTTTATCTAGCAAT  
 TCTGTTGGGCAACTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA  
 TGTACTTTCTGCTTGCAAACCTGTCATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT  
 AAAATGATTGCAGACTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC  
 40 AGATTTTCTTTGTTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT  
 GACCGTTATGTTGCTATATGCAAACTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT  
 GTGTTGTGCTCGTCTCATTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA  
 TCACTGTTAATCTGCCATTTTGTGGTCTAATAAGGTAGACAGTTTTTTCTGTGACCTTCC  
 TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTCAGCTTACTAATAGTTGCAGAT  
 45 AGTGGCTTTCTTTCTCTGAGTTCCTTTCTCCTCTTGGTTGTCTCCTACACTGTAATACTTGT  
 ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA  
 TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT  
 TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCTGT  
 AATCTACACGCTAAGAAACAAAGAAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA  
 50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA  
 (SEQ ID NO: 410).

**AOLFR220 sequences:**

MKQYSVGNQHSNYRSLFPFLCSQMTQLTASGNQTMVTEFLFSMFPHAHRGGLLFFIPLLLIYG  
 55 FILTGNLIMFIVIQVGMALHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF  
 HSLGITESCULTAMAIDRYAICNPLRYPTIMIPKLICIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIIVILGMHSAEGHHKAFST  
CAAH LAVFLFFGSVAVMYLRFSATYSVFWDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF  
HYQKRAGWAGK (SEQ ID NO: 411).

- 5 ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTTCCTTTTCT  
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCTT  
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCTTGCTTCTCA  
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTCAATTGTCATCCAGGTGGGCATGGC  
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCTCTCTGGAGATCTGCTATACCA  
10 CAACCACCATCCCCAAGATGCTGTCTGCCTAATCAGTGAGCAGAAGAGCATTTCGGTGGC  
TGGCTGCCTCCTGCAGATGTACTTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCCTG  
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA  
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTGTGGCTTCTCCTTG  
CTTCTGAGATTGCATGGATTTCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT  
15 ATTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTAGTGGTCATT  
GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCCTGGTCATTGCTCTATCCTACA  
TCCGGATTATTATAGTGATTCTGGGAATGCACCTCAGCTGAAGGTCATCACAAGGCCTTTTC  
CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTTGGCAGTGTGGCTGTCATGTATT  
TGAGATTCTCAGCCACCTACTCAGTGTTTTGGGACACAGCAATTGCTGTCACTTTGTATC  
20 CTTGCTCCCTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA  
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:  
412).

**AOLFR221 sequences:**

- 25 MRNLSGGHVEEFVLVGFPTTPPLQLLLFLVFFAIYLLTLENALIVFTIWLAPSLHRPMYFFLGH  
LSFLELWYINVTIPRLAAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP  
LLYPSLMPSSLATRLAAASWGSFFSSMMKLLFISQLSYCGPNIINHFFCDISPLNLTCSDKEQA  
ELVDFLLALVMILLPLLA VVSSYTAIIAAILRIPTSRGRHKAFSTCAAH LAVVIYSSSTLFTYAR  
PRAMYTFNHNKIISVLYTIIVPFFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID  
30 NO: 413).

- ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC  
CTCCCTCCAGCTGCTCCTCTTTGTCTTTTTTTTGCAATTTACCTTCTGACATTGTTGGAGA  
ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTTC  
35 CTTGGCCATCTCTCTTCTGAGCTATGGTACATCAATGTCAACCTCCTCGGCTCTTGGC  
AGCCTTTCTTACCCAGGATGGTAGAGTCTCTACGTAGGTTGCATGACCCAACTGTACTTC  
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT  
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG  
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGTCCATGATGAAGCTTCTTTTATTTCCCAA  
40 TTGTCTACTGTGGACCCAACATTATCAACCCTTTTTCTGTGATATTCCCCACTACTCAA  
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCTTCTGGCCCTGGTGATG  
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACTGCCATCATTGCAGCCATCCTGAG  
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG  
GTTGTTATCTACTACTCCTCACTCTCTTACCTATGCACGGCCCCGGGCCATGTACACCTT  
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA  
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGCCTTCAGGAAGACAGTGATGGGCAGAT  
GTCATATCCTAGGGATGTTCAAGGACTGA (SEQ ID NO: 414).

**AOLFR222 sequences:**

- 50 MGQTNVTSWRDFVFLGFSSSGELQLLL FALFLSLYLVTLT SNVFIIAIRLDSHLHTPMYFLSFL  
SFSETCYTLGIIPRMLSGLAGGDQAISYVGCAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL  
HYASHMNP TLCAQLVITSFLTGYLFGMLTVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS  
ELRIFILSLLVLLVSFFITISYAYILAILRIPSAEGQKKAFSTCASHLTVVIIHYGCASFVYLRPK  
ASYSLERDQLIAMTYTVVTPLLNPIVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTGTTGCTTCCTGGGCTTCTCCAGTTCTG  
 GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTTCTCTCTGTATCTAGTCACTCTGACCAGC  
 AATGTCCTTATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCCATGTACCTCTT  
 CCTTTCCTTCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT  
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT  
 TTCTGCCTCATGGGCCTGTACTAAGTGCCTTCCTTCTGGCTGCCATGGGCTTIGACAGATATG  
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCTCTGTGCCAGCT  
 GGTCACTACTTCTTCTGACTGGATACCTCTTGGACTGGGAATGACACTAGTTATTTCC  
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG  
 10 AGCCTAGCCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTATCCTCAGTCTTTTGG  
 TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG  
 AGGATCCCTCTGCTGAGGGGCAGAAGAAGGCCTTCTCCACTTGTGCTCGCACCTTACAG  
 TGGTCATTATTATTATGGCTGTGCTTCTTTCGTGTACCTGAGGCCCAAAGCCAGCTACTCT  
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA  
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG  
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

#### AOLFR223 sequences:

MEAANESSEGISFVLLGLTSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA  
 20 HLSFADLCFASVTVPKMLANLLAHDHSISLAGCLTQMYFFFALGVTDSCLLAAMAYDCYVAIR  
 HPLPYATRMSRAMCAALVGMALVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLRLSC  
 SDTHHIQLLIFTEGAADVTPFLILASYGAIAAAVLQPSASGRRLRAVSTCGSHLAVVSLFYGT  
 VIAVYFQATSRRAEWGRVATVMYTVVTPMLNPIHYSLWNRDVQALRALLIGRRISASDS  
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTTCGTTTTATTGGGACTGACAACAA  
 GTCCTGGACAGCAGCGGCTCTCTTTGTGCTGTTCTTGTCTTGTATGTGGCCAGCCTCCTG  
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT  
 TCCTGCTGGCCACCTGTCTTTGCTGACCTCTGTTTCGCCTCCGTCACTGTGCCAAAGATG  
 30 TTGGCCAACTTGTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT  
 ACTTCTTCTTTGCCCTGGGGGTAAGTATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG  
 CTACGTGGCCATCCGGCACCCCTCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA  
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCACGTCCACTCCCTCCTGTATATCCTGCTCA  
 TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCACTTCTTCTGTGACCACAGCCT  
 35 CTCTTAAGGCTCTCGTGCTCTGACACCCACCATCCAGCTGCTCATCTTACCGAGGGCG  
 CCGCAGTGGTGGTCACTCCCTTCTGTGCTTCCCGGGCTGTGTCCACCTGTGGCTCCAC  
 CGTGCTGCTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC  
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTATGTACACTGTAGTACCCCCATGC  
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT  
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

#### AOLFR224 sequences:

MGSFNSTSFEDGFILVGFSDWPQLEPILFVIFIFYSITLFGNTHIALSWLDLRLHTPMYFFLSHLSL  
 45 LDLCFTTSTVPQLLINLCGVDRITITRGGCVAQLFIYALGSTECVLLVVMFAFDYAAVCRPLHY  
 MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT  
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTGSHLLVFLFYGSAIYT  
 YLQSIHNYSEREGKFVALFYTIITPILNPLYTLRNKDVKGALWKVLWRGRDSG (SEQ ID NO:  
 419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC  
 CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTACTCCCTAACTCTCTTTGGC  
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT  
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTACCACACAGCACCGTGCCCCAGCTCCTGA  
 55 TCAACCTTTGCGGGGTGGACCGCACCATACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT  
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGATGGCCTTTGACCGCTAT

GCTGCTGTCTGTCTGCTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCT  
 GGCTATCGCCTCCTGGGGTGCGGGTTTCGTGAACCTCTCTGATCCAGACAGGTCTCGCAATG  
 GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA  
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCCGAGTCATAGT  
 5 CGTGGCTGTTCTGTCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG  
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA  
 GTAGTTTTCTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC  
 TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTATACTATAATTACCCCCATTCTCAATCCTC  
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG  
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

**AOLFR225 sequences:**

MENYNQTSTDFILLGLFPPSIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID  
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMA YDRYIAICFPLHYLRM  
 15 SKRVCVLMITGSWIIGSINACAHTVYVLHPIYCRSRAINHHFCDVPAMVTLACMDTWVYEGTV  
 FLSATIFLVFPFIGISCSYGQVLFVAVYHMKSAEGRKAYLTCSTHLTVVTFYAPFVYTYLRPRS  
 LRSPTEDKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA  
 20 TAATTGACCTTTTCTTCTTCTCATTCTCATTGTTTTCATTTTCCTGATGGCTCTAATTGGAAACG  
 TGTCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCTACTG  
 AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTTGTTCTTAAGATGGCATCTGA  
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTCAGAGTTTCTTCTTCT  
 TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC  
 25 TATTTGCTTTCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA  
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA  
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCAGCAATGGTGACT  
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGTTTTTGAGTGCCACCATCTTTC  
 TCGTGTTCCTTTCATTGGTATTTTCATGTTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC  
 30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA  
 GTAACCTTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC  
 AACAGAGGACAAGGTTCTGGCTGTCTTCTACCATCTCCTCACCCCAATGCTCAACCCCATC  
 ATCTATAGCCTGAGGAACAAGGAGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC  
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

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**AOLFR226 sequences:**

MEWRNHSGRVSEFVLLGFAPAPLQVLLFALLLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL  
 ANMSFLEIWYVTVTIPKMLAGFVGSQDGHGLISFEGCMTQLYFFLGLGCTECVLLAVMAYD  
 RYMAICYPLHPVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL  
 40 NLSCDTMSTAELTDFILAFILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLTVVIF  
 YAASIFIYARPKALSAFDTNKLVSVLYAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP  
 KKASRNV (SEQ ID NO: 423).

ATGGAGTGCGGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT  
 45 CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGTGCTGGCCTATGTGTTGGTGCTGAC  
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCTCCACAAACCCATGTAC  
 TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT  
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC  
 ATGACACAGCTCTACTTTTTCTTGGCTTGGGCTGCACTGAGTGTGTCCTTCTCGTGTTAT  
 50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCACTGGCC  
 GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTGGCATCTCCATGGTCAA  
 AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG  
 ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTCT  
 ATCCTGGCCATTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT  
 55 TACTGGTGCTGTGATGCACATATCTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT  
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTA CTGTATGCTGTCAATTGTA  
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT  
GTA CTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA  
G (SEQ ID NO: 424).

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**AOLFR227 sequences:**

MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTHIGNVVIITVVSQGLRLHSPMYMFLQH  
LSFLEVWYTSTTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP  
LRYPFMLHRGLCARLVVVSCTGVSTGFLHSMISRLDFCGRNQINHHFFCDLPPLMLQSCSRV  
10 YITEVTIFILSIAVLCICFFLTLPYVFISSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMIV  
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF  
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTTCACTGTTAGGATTCCAGAACCTTC  
15 TTGAATGGCAGGCCCTGCTCTTTGTCAATTTTCTGCTCATCTACTGCCTGACCATTATAGGG  
AATGTTGTCAATCATACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCTATGTACATGT  
TCCTCCAGCATCTCTCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCCCTTCTCCTA  
GCCAACCTGCTGTCTCTGGGGCCAAGCCATCTCTTCTCTGCTGCATGGCACAGCTCTACT  
TCTTCGTATTCTCGGCGCCACCGAGTGCTTTCTCTGGCCTTCATGGCCTATGACCGTTAC  
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGT  
GGTGGTGGTCTCATGGTGCACAGGGGTGACACAGGCTTTCTGCATTCCATGATGATTTC  
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA  
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC  
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTTATTGTGTCTCTCCATATT  
25 GAGAATCCCTTCCACCTCTGGCGGAGAAAGACCTTTTCCACATGTGGCTCCACCTGGCT  
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCAGTCCCCACCTGTT  
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTCACACCACTGCTGAACCCA  
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG  
AAATGTGGTATTCTATGGAGTACAAGTAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

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**AOLFR229 sequences:**

MFYVNQIPFQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK  
IILIHDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE  
FLLGLMSCDRYVAICNPLHYPDLMRSKICWLIVAAAWLGGSIDGFLTPVTMQFPFCASREIN  
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRRKAVAT  
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTLTPMLNPLIYSLRNKDVGTALQK  
VVGRCVSSGKVTTT (SEQ ID NO: 427).

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTATCATATCTCTTTCGTGTACCCTACAGA  
40 GCTATGGAGCAGAGCAATTATTCGGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA  
ACGCCCCGTTTCCCCTGGCTTCTTTGCCCTCATTCTCCTGGTCTTTGTGACCTCCATAGCCAG  
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCATGTACTTC  
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTCCACCATTGTGCCCAAAATGCT  
GGTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTC  
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCTGTGATCGCTA  
CGTAGCCATCTGCAACCCTCTGCACTATCTGACCTCATGAGCCGCAAGATCTGCTGGTTG  
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTACCCCGTCACCA  
TGCAGTTCCCTTCTGTGCTCTCGGGAGATCAACCACTCTTCTGCGAGGTGCCTGCCCTT  
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGTGATTATTA  
50 TGATGCTCCTCATCCCTTTCTGTGTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT  
TATAGGATGAGCGAGGCAGAGGGGAGGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG  
GTGGTTGTGACCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA  
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT  
CCTACTATTTACAGCCTTAGGAACAAGGATGTACGGGGGCCCTACAGAAGGTTGTTGGG  
55 AGGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

**AOLFR230 sequences:**

MGMEMLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMSRLHTPMYFLLS  
 QLSIMDTIYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTLIGGEFFLLGLMAYDRYVAVCNP  
 LRYPLLMNRRVCLFMVVGSWVGGSLDGFM LTPVTMSFFPCRSEINHFFCEIPAVLKLSCDTDS  
 5 LYETLMYACCVLM LLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVS VFYGAIFY  
 TNVLPHSYHTPEKDKVVS AFYTILTPMLNPLIYSLRNKDVAALRKVLGRGSSQSIRVATVIR  
 KG (SEQ ID NO: 429).

10 ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC  
 ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA  
 GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT  
 CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC  
 TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCTTCTCTGGGCTGTGCAGTTCAGATCTT  
 CCTCTACCTGACCTGATTGGAGGGGAATTCTTCTGCTGGGTCTCATGGCCTATGACCGC  
 15 TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT  
 CATGGTGGTCGGCTCCTGGGTTGGTGGTTCCTTGGATGGGTTTCATGCTGACTCCTGTCACT  
 ATGAGTTTCCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTCTGTGAGATCCCAGCCGT  
 GCTGAAGTTGTCTTGACAGACACGTCATCTATGAGACCCTGATGTATGCCTGCTGCGTG  
 CTGATGCTGCTTATCCCTCTATCTGTCTCTGTCTCCTACACGCACATCCTCCTGACTGT  
 20 CCACAGGATGAACCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCTCCACATT  
 ATGGTGGTGAGCGTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC  
 AACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTACCCCCATGCTCAA  
 CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG  
 GAGATGTGGTTCCTCCCAGAGCATCAGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID  
 25 NO: 430).

**AOLFR231 sequences:**

MERANHSVVSEFILLGLSKSQNLQILFFLGFSVVFVGVILGNLLILVTVTFDSLHTPMYFLLSNL  
 SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMAIDRYVAICKP  
 30 LHYMTIMSPRVL TGLLLSSYAVGVFHSSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI  
 LQLLVIADSGLLSLVCFLLLLVSYGVII FSVRYRAASRSSKAFSTLSAHITVVTLFAPCVFIYVW  
 PFSRYSVDKILSVFYTIFTPLNPIIYTLRNQEVKAAIKKRLCI (SEQ ID NO: 431).

35 ATGGAAAGAGCAAACCATTTCAGTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC  
 AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA  
 AACCTGCTCATCTTGGTGACTGTGACCTTTGATTGCTCCTTCACACACCAATGTATTTCT  
 GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGTACCCCTAAGATGATTG  
 TAGATTTCTCCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATCCAGATGTTCTT  
 TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT  
 40 GTTGCCATATGCAAAACCCCTCCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC  
 TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTCATGTTG  
 ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTCTGTGACCTTCCCCTTGTGAT  
 TAAACTTGCCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC  
 CTGTCACTGGTCTGCTTCTCCTCTTGGTGTCTCCTATGGAGTCATAATATTCTCAGTTAG  
 45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG  
 TGACTCTGTTCTTTGCTCCGTGTGCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA  
 GATAAAATTCTTTCTGTGTTTACACAATTTTCACACCTCTCTTAAATCCTATTATTTATAC  
 ATTAAGAAATCAAGAGGTAAAAGCAGCCATTAAAAAAGACTCTGCATATAA (SEQ ID NO:  
 432).

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**AOLFR232 sequences:**

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV  
 VIFVVFLMALSGNAVLILLIHCD AHLHTPMYFFISQLSLMDMAYISVTVPKMLLDQVMGVNKIS  
 APEGCMQMFFYVTLAGSEFFLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD  
 55 GFTFTPTMTFPFRGSREIHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLM LLIPIVVISSSYLLILL



TIHGMNSAEGRKKAFAATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDDMMVSVFYTILTPVVNP  
LIYSLRNKDVMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTCATCCTGATGGGAC  
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG  
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG  
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACA  
CTGTGACGCCCCACCTCCACACCCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA  
10 TGGCGTACATTTCTGTCACTGTGCCAAGATGCTCCTGGACCAGGTTCATGGGTGTGAATAA  
GATCTCAGCCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTCAGAA  
TTTTCTCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA  
CCCTGTCCTCATGAACCATAGGGTGTGTCTTCTCTGTCATCAGGCTGCTGGTTCCTGGGCT  
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGGA  
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC  
15 TCTATGAGATTTTCATGTACTTGTGCTGTGTCTCATGCTCCTCATCCCTGTGGTGATCATT  
TCAAGCTCCTATTTACTCATCCTCCTCACCATCCACGGGATGAACTCAGCAGAGGGCCGGA  
AAAAGGCCTTTGCCACCTGCTCCTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC  
ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG  
TCTTCTATACCATCCTCACTCCAGTGGTGAACCCCTTAATCTATAGTCTTAGGAATAAGGAT  
20 GTCATGGGGGCTCTGAAGAAAATGTTAACAGTGAACCTGCCTTTCAAAAAGCTATGGAG  
TAG (SEQ ID NO: 434).

**AOLFR233 sequences:**

25 MANITRMANHTGKLDFFILMGLFRRSKHPALLSVVIFVFLKALSGNAVILLIHCD AHLHSPMY  
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR  
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHHFFCEVPAVTI  
LSCSDTSLYETLMYLCCVLMMLIPVTIISSSYLLILLTVHRMNSAEGRKKAFAATCSSHLTVVILFY  
GAAVYTYMLPSSYHTPEKDDMMVSVFYTILTPVLNPLIYSLRNKDVMGALKKMLTVRFVL  
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAGGATGGCCAACCACACTGGAAAAGTTGGATTTTCATCCTCATGGGAC  
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAAG  
GCGTTGTCTGGAAATGCTGTCTGATCCTTCTGATACTGTGACGCCCCACCTCCACAGCC  
CCATGTACTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG  
35 CCCAAGATGCTCCTGGACCAGGTCAATGGGTGTGAATAAGGTCTCAGCCCCTGAGTGTGGG  
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTTCGGAATTTTTCTTCTAGCCACCATGGC  
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCTCATGAACCATAGG  
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTTCCTGGGCTCAGTGGATGGCTTCATGCTCAC  
TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG  
40 TCCCTGCTGTAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCCTCATGTACCTA  
TGCTGTGTCTCATGCTCCTCATCCCTGTGACGATCATTTCAAGCTCCTATTTACTCATCCT  
CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCCGGA AAAAAGGCCTTTGCCACCTGCTC  
CTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA  
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC  
45 GGTGCTGAACCCCTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA  
ATGTTAACTGTGAGATTCGTCCTTTAG (SEQ ID NO: 436).

**AOLFR234 sequences:**

50 MPNSTTVMEFLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTTCDSSLHMPMYFFLRN  
LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVVFVYVELLFTIMAHDRYVAVCQPL  
HYPVIVNSRICQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLLKLSCSDTFSNE  
VMIVVSALGVGGGCFIFIIRSYIHIFSTVLGFPGRADRTKAFSTCIPHILVSVFLSSCSSVYLRPP  
AIPAATQDLILSGFYSIMPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC  
TACAGATTTTACATTCTGCATCCTTCTTTATGTTGTATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG  
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT  
 CCCTACTGGACAGCACCACCATTTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT  
 TTTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG  
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT  
 GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG  
 CCCTTCTGTGCGGTCCAACGTTATTCATCAAATCTTCTGTGACATCCCCTCTCTGCTGAAGCT  
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT  
 GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGTGCTCGGGTT  
 10 TCCAAGAGGAGCAGACAGAAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG  
 TCAGTCTTCCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC  
 CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCTCTTTAACCTATTATTTA  
 CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAAATTTTTTA  
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

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**AOLFR235 sequences:**

MDGVNDSSLQGFVLMGISDHPQLEMIFFIAILFSYLLTLLGNSTIILSRLEARLHTPMYFFLSNL  
 SSLDLAFATSSVPQMLINLWGPKTISYGGCITQLYVFLWLGATECILLVVMADFVAVCRPL  
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL  
 20 NQAVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVVFIFYGSASYGY  
 LLPAKNSKQDQGFISLIFYSLVTPMVNPLIYTLRNMEVKGALRRLGKGREVG (SEQ ID NO:  
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC  
 25 CCCAGCTGGAGATGATCTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCTACTTGGG  
 AACTCAACCATCATCTTGCTTTCCCGCCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT  
 CCTCAGCAACCTCTCCTCCTTGACCTTGCTTTCGCTACTAGTTCAGTCCCCAAATGCTGA  
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT  
 CTTCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC  
 30 GTGGCAGTGTGCCGGCCCTCCGCTACACCGCCATCATGAACCCCAAGCTCTGCTGGCTGC  
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT  
 GCAGCTCCCATTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT  
 GATCAAACTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC  
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT  
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT  
 GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC  
 AGCAAACAGGACCAGGGCAAGTTCATTCCCTGTTCTACTCGTTGGTCACACCCATGGTGA  
 ATCCCCTCATCTACAGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG  
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

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**AOLFR236 sequences:**

MTSQERDTAIYSINVSFVAKGMTSRVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL  
 LFLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSTVTVPKVMAGLLTLDGKVIS  
 FEGCAVQLYCFHFLASTEFLYTVMAYDRYLAICQLHYPVAMNRRMCAEMAGITWAIGATH  
 45 AAIHTSLTFRLLYCGPCHIAFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLLIVISYIFIVA  
 AVLIRTAQGRQRAFSPCTAQLTGVLVYVPPVCIYLQPRSEAGAGAPAVFYTIVTPMLNPFY  
 TLRNKEVKHALQRLLCSSFRETAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG  
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA  
 CTGTGGTGAGCCACTTCTTCCTGGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT  
 CTTCTCCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCTCCTAA  
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCATGTACCACTTCTGGGGCACCTCTCCTTC  
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCCTGCTGACTCTGG  
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC  
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC  
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT  
 GTGGGCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCCTGTCTAAAGCTCGCCTGT  
 ACAGACACCACCATTAAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT  
 5 GCCTCATCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA  
 GCCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT  
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC  
 CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCACTTTACACTTTGCGGA  
 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTCCGAGAGTCTACAG  
 10 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

**AOLFR237 sequences:**

MDQRNYTRVKEFTFLGITQSRELSQVLFITFLVYMTTLMGNFLIMVTVTCEHLHTPMYFLL  
 RNLSILDICFSSITAPKVLIDLLSEKTSFSGCVTQMFFFHLLGGADVFSLSVMAFDRYIAISKPL  
 15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCGPVLDTFYCDVPQVLKACTDTFT  
 LELLMISNGLVSWFVFFLLISYTVILMLRSHTGEGRRKAISTCTSHITVTVLHFVPCIVVYA  
 RPFTALPTDTAISVTFTVISPLNPIYTLRNQEMKMLAMRKLKRRLGQSERILIQ (SEQ ID NO:  
 443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC  
 GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG  
 AAACCTTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC  
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCCTG  
 ATAGATCTTCTATCAGAGACAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT  
 25 TCTTCCACCTTCTGGGGGGAGCAGACGTTTTTCTCTCTGTGATGGCGTTTGACCGCTAT  
 ATAGCCATCTCCAAGCCCCTGCACTATAAGACCATCATGAGTAGGGGGCGATGCACAGGCC  
 TCATCGTGGGCTTCTGGGTGGGGGGCTTGCCACTCCATAGCGCAGATTTCTCTATTGCT  
 CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCC  
 TCAAACCTGCCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT  
 30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA  
 GGTCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACCG  
 TGGTGACCTGCAATTCGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCC  
 ACAGACACTGCCATCTCTGTACCTTCACTGTCTATCTCCCTTTGCTCAATCCTATAATTTA  
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAACTGAAGAGACGGCTAGGAC  
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

**AOLFR238 sequences:**

MAPENFTRVTEFILTVSSPELQIPLFLVFLVLYVLTMAAGNLGIITLTSVDSRLQTPMYFFLRHL  
 AIINLGNSTVIAPKMLMNFLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP  
 40 LLYMVVVSRRCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFYCDIAPLLALSCSDTYIPE  
 TIVFISAATNLFFSMITVLVSFYFNIVLSILRIRSPGRKKAFSTCASHMIAVTVFYGTMLFMYLQP  
 QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:  
 445).

45 ATGGCTCCTGAAAATTTACACAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC  
 CAGAGCTCCAGATTCCTCTCTCTGGTCTTCTAGTGTCTATGTGCTGACCATGGCAGG  
 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT  
 TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCAATTGCCCTAAAATGCTG  
 ATGAACCTTTTAGTAAAGAAAGAAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG  
 50 GGTTCTTGTTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA  
 TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGC  
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCACTTGTATATTC  
 TCTGTGTCTTATTGCTCTTCTAATATAATCAATCAATTTTACTGTGATATTGCACCTCTGTT  
 AGCATTATCTTGCTCTGATACTTACATACCAGAAACAATAGTCTTTATATCTGCAGCAACA  
 55 AATTTGTTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA  
 AGGATACGTTACACAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT  
 CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCCTATGCTGAATCC  
 CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAAT  
 CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

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**AOLFR239 sequences:**

MDPQNYSLVSEFVLHGLCTSRHLQNFFIFFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG  
 NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQAIFFLHFTGGAEMVLLVSMAYDRYVAIC  
 KPLHYMTLMSWQTCIRLVLASWVVG FVHSISQVAFVNLPCGPNEVDSSFCDLPLVIKLACM  
 10 DTYVLGHIMISDSGLLSLSCFLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV  
 YVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTCAGAAATTTGTGTTGCATGGACTCTGCACTTCAC  
 GACATCTTCAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT  
 15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT  
 CCTGCTGGGGAACCTAGCTTTCTGGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG  
 ATCAGGGATTTCTTAGTGATCAAAACTCATCTCCTTTGGAGGATGTATGGCTCAAATCT  
 TCTTCTTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG  
 ATATGTGGCCATATGCAAACCCTTGCAATACATGACTTTGATGAGTTGGCAGACTTGCATC  
 20 AGGCTGGTGCTGGCTTCATGGGTCGTTGGATTTGTGCACTCCATCAGTCAAGTGGCTTTCA  
 CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG  
 GTGATCAAACCTTGCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG  
 GGTTGCTTTCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT  
 ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA  
 25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTGTATGTGCGGCCTTTCACTAGGTTT  
 TCTGTGGACAAGCTGCTGTCTGTGTTTTATACCATTTTACTCCACTCCTGAACCCCATAT  
 CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT  
 GACTTTTCAATGA (SEQ ID NO: 448).

30 **AOLFR240 sequences:**

MAGENHTTLPEFLLLGFSDLKALQGFLFWVVLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR  
 QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCAAQMYVFIVLGISECCLLTAMAYDRYVAIC  
 QPLRYSTLLSPRACLAMVGSSWLTGIITATTHASLIFSLPFRSHPIIPHFLCDILPVLRLASAGKHR  
 SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRKVFSTCSSHLLVVSLLFGTASITYIRPQ  
 35 AGSSVTTDRVLSLFYTVITPMLNPIIYTLRNDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA  
 AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG  
 40 TAACTCCCTGATCATCCTCCTCACACAGGTGAGCCCTGCCCTGCACTCCCCATGTACTTCT  
 TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCCT  
 GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCAGATG  
 TACGTCTTCATTGTCCTGGGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC  
 GATATGTTGCCATCTGCCAGCCCCCTACGCTATTCCACCCTCTTGAGCCACGGGCCTGCTT  
 GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC  
 45 ATCTTCTCTCTACCTTTTCGACGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC  
 AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC  
 CATAGTCTTCATTATGATCCCTTCTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG  
 CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA  
 TCTGCTCGTGGTCTCTCTCTTTGGAACAGCCAGCATCACCTACATCCGGCCGAGGCA  
 50 GGCTCCTCTGTTACCACAGACCGCGTCTCAGTCTCTTCTACACAGTCATCACACCCATGCT  
 CAACCCCATCATCTACACCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT  
 GAAGAGGCAGCGCCCCCTCACCTGA (SEQ ID NO: 450).

**AOLFR241 sequences:**

55 MPQILIFTYLNMFYFFPPLQILAENLTMVTEFLLGFFSLGEIQLALFVVFLLYLVLVLSGNVTIIS  
 VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAAACAIGGFLASLTVVNLVFSLPFCSANKVNH  
YFCDISAVILLACTNTDVNEFVIFCGVLVLVVPFLFICVSYLCILRTLKIPSAEGRKAFSTCAS  
HLSVVIVHYGCASFYLRPTANYVSNKDRLVTVTYITVTPLLNPMVYSLRNKDVQLAIRKVLG  
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT  
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTTCCAGCCTTGGT  
GAAATTCAGCTGGCCCTCTTGTAGTTTTCTTTTTCTGTATCTAGTCATTCTTAGTGGCAA  
TGTCACCATTATCAGTGTCACTCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC  
10 TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCATTCTACCCAAGATGCTCATC  
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAAATGTTCTTCTT  
CCTTGGTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTATGATCGCTATGCTG  
CCATTTGTCAACCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAAACCTGGC  
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTTCAGCC  
15 TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT  
CTGGCTTGTACCAACACAGATGTTAACGAATTTGTGATATTCATTTGTGGAGTTCTTGTAC  
TTGTGGTTCCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG  
ATTCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCTCTCACCTCAGTGTG  
TTATTGTTTATTATGGCTGTGCTTCTTCTATCTACCTGAGGCTACAGCAAACTATGTGTCC  
20 AACAAAGACAGGCTGGTGACGGTGACATACACGATTGTCACTCCATTACTAAACCCCATG  
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTGGGCAAGAAA  
GGTTCTCTAAACTATATAATTGA (SEQ ID NO: 452).

#### AOLFR242 sequences:

25 MNTTLFHPYSFLLLGIPLGLESMLHWVGFPPFAVFLTAVLGNTTLFVIQTDSSLHHPMFYFLAILS  
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY  
TLVLTKNVVSVMALAJFLRPLVFVFPVLFILRLPFCGHQIIPHTYGEHMGRIARLSCASIRVNIYG  
LCAISILVFDIIAIVISYVQILCAVFLSSHDARLKAFTCSHVCVMLTFYMPAFFSMTHRFGR  
NIPHFHILLANFYVVIPALNSVIYGVRTKQIRAQVLKMFNFK (SEQ ID NO: 453).

30

ATGAATACCACTCTATTTTCATCCTTACTCTTTCCTTCTTCTGGGAATTCCTGGGCTGGAAAG  
TATGCATCTCTGGGTTGGTTTTCTTTCTTTGCTGTGTTCCCTGACAGCTGTCCTTGGGAATA  
TCACCATCCTTTTTGTGATTACAGCTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTCTG  
GCCATTCTGTCACTATTGACCCGGGCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC  
35 CTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTCATCC  
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC  
CATCTGTGACCCCTCTTGTCTACACGTTGGTGTGACAAACAAGGTGGTGTGAGTTATGGCA  
CTGGCCATCTTTCTGAGACCCCTTAGTCTTTGTCTATACCCTTTGTTCTATTATCCTAAGGCT  
TCCATTTTGTGGACACCAAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCGC  
40 CTGTCTTGTGCCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT  
CTTGACATCATAGCAATTGTCAATTCCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT  
CTTCACATGATGCACGACTCAAGGCATTACAGACCTGTGGCTCTCATGTGTGTGTCATGTT  
GACTTTCTATATGCCTGCATTTTTCTCATTCATGACCCATAGGTTTGGTCGGAATATACCTC  
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA  
45 ATTTATGGTGTGACAACCAACAGATTAGAGCACAAGTGCTGAAAATGTTTTTCAATAAAT  
AA (SEQ ID NO: 454).

#### AOLFR243 sequences:

MEQVNKTVVREFVVLGFSSRLRLQQLLFVIFLLLYLFTLGTNAIISTIVLDRALHTPMYFFLAIL  
50 SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLAAMGYDRYMAICNPLR  
YSVLMGHGVCMLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVKLKASQHSF  
SQLVIFMLGVFALVPLLLILVSYIRIISAILKIPSSVGRYKTFSTCASHLIVTVHYSCASFIYLRPK  
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRRTIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG  
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT  
 CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCATTGTACCCAAGATGCTGG  
 TTGACCTGCTGTCCAGAAAGAAGACCATTTCTTCTGCTGGGCTGTGCCATCCAAATGTTTTCC  
 TTCTCTTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGCTATGATCGCTATAT  
 5 GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA  
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCAACACCTCCCTAGTATTTCA  
 TCTGCCCTTCCACTCCTCCAACCAGTCCATCACTTCTTCTGTGACATCTCCCCTGTCCCTA  
 AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTCATGCTTGGTGTATTTGC  
 CTTGGTCATTCTCTGCTACTTATCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA  
 10 AAATCCCTTCTCCTCGTTGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG  
 GTAAGTGTTCATACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC  
 AAGCCAAGACACCCTAATATCTGTGTCATACACCATCCTTACCCCATTTGTTCAATCCAATG  
 ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAAACAATCGGCCAAACT  
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

**AOLFR244 sequences:**

MWQEYYFLNVFFLLKVCCLTINSHVILLPWECYHLIWKILPYIGTTVGSMEYNTSSTDFTF  
 MGLFNRKETSGLIFAIISIFFTALMANGVMIFLIQTDRLRLHTPMYFLLSHLSLIDMMYISTIVPKM  
 LVNYLLDQRTISFVGCTAQHFLYLTLVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI  
 20 IAGSWFGGSLDGFLLPITMSFPFCNSREINHFFCEAPVLKLACADTALYETVMYVCCVLMMLL  
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSIFYGAAMYTYMLPHSYHKPAQ  
 DKVLSVFYITLTPMLNPLIYSLRNKDVGTGALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCCTTTTAAAAGTTTGCTGCCTAAC  
 25 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT  
 TACCTTATATCGGCACAACCTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT  
 CACTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTGGCATCATCTCT  
 ATCATCTTCTTCAACGCCTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT  
 TGCGCCTTCATACACCCATGTACTTCTCCTCAGCCACCTTTCTTAAATTGACATGATGTAT  
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCTCT  
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCTCTG  
 CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTGCAACCCTCTGAGATACCCTGTCC  
 TCATGAGCCGCCGGTCTGTTGGATGATTATAGCAGGTTCTGGTTTGGGGGCTCTTTGGA  
 TGGCTTCTCTCTAACCCCATACCATGAGCTTTCCCTTCTGCAATTCCCGGGAGATTAAACC  
 35 ACTTCTTCTGTGAGGCACCAGCAGTCCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA  
 GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTTCTCTGTAGTCCTTGCTT  
 CCTATGCCCGAATCCTGACTACAGTTCAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG  
 CATTGCCACTTGCTCATCCACATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC  
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCCTCTCTGTGTTTT  
 40 ACACCATCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC  
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT  
 CTTTGA (SEQ ID NO: 458).

**AOLFR245 sequences:**

MDLKNGLSVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCTSTLHSPLYFLLGN  
 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLIIMAFDRYVAICKP  
 LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMLNLPFCGHNVINNIFCDLPLVIKLACIETYTLE  
 LFVIADSGLLSFTCFILLVSVYIVLVSPVKSSHGLSKALSTLSAHIIIVTLFFGPCIFIYVWPFSSL  
 ASNKTAVFYTVITPLLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

50

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT  
 GGGAACCTCAAATTTTCTTCTTTGTGACATTTCCCTGATCTACGGTGCTACTGTGATGGGA  
 AACATTCTCATTATGGTCAAGTGACATGTAGGTCAACCTTCATTCTCCCTGTACTTTCT  
 CCTTGGAATCTCTCTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA  
 55 TAGATTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT  
 CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG  
 TTTGCGATACTTTTCATGGATAATTGGTTTTTTTACACTCCATAAGCCAGATAGTTTTAACAAT  
 GAACTTGCCCTTTCTGTGGCCACAATGTCATAAACAACATATTTTGTGATCTTCCCCTTGTGA  
 TCAAGCTTGCTTGCATTGAAACATACACCCTGGAATTATTTGTCATTGCTGACAGCGGGCT  
 5 GCTCTCTTTCACCTGTTTCATCCTCTTGCTTGTTTTCTTACATTGTCATCCTGGTCAGTGTACC  
 AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCACATCATTGTG  
 GTCACCTCTGTTCTTTGGACCTGTATTTTTATCTATGTTTGGCCATTGAGTAGTTTGGCAAG  
 CAATAAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA  
 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT  
 10 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

#### AOLFR246 sequences:

MSPENQSSVSEFLLLGLPIRPEQQAVFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH  
 LALTDISFSSVTPKMLMDMRKYKSILYEECISQMYFFIFFDLDSFLITSMAYDRYVAICHPL  
 15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLLRLSFCAANTIPHVFCDLAALLKLSCSDIFLNE  
 LVMFTVGVVVITLPMCLVSYGYIGATILRVPSTKGIHKALSTCGSHLSVVSLLYYGSIFGQYLF  
 PTVSSIDKDVIVALMYTVVTPMLNPFYISLRNDRMKEALGKLFSRATFFSW (SEQ ID NO:  
 461).

20 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC  
 CAGAGCAGCAGGCTGTGTTCTTACCCTGTTCTGGGCATGTACCTGACCACGGTGTGGG  
 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTCACCTTACACCCCCATGTACTTCT  
 TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG  
 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT  
 25 TTTTATATTTTTACTGACCTGGACAGCTTCTTATTACATCAATGGCATATGACCGATAT  
 GTTGCCATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT  
 AGTGGCTGTATCTTGGATTCTGTCTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC  
 GGCTGTCTTTCTGTGCTGCGAACACCATCCCCCATGTCTTCTGTGACCTTGCTGCCCTGCTC  
 AAGCTGTCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTACAGTAGGGGTGGTGG  
 30 TCATTACCCTGCCATTTCATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG  
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG  
 TGGTGTCTCTTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCGACTGTAAGCAGTTCT  
 ATTGACAAGGATGTCATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT  
 TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG  
 35 CAACATTTTTCTCCTTGGTGACATCTGACTTTTTAAAAAATTAG (SEQ ID NO: 462).

#### AOLFR247 sequences:

MGQHNLTVLTEFILMELTRRPELQIPLFGVFLVIYLLITVVGNLTMILTKLDSHLHTPMYFSIRHL  
 ASVDLGNSTVICPKVLANFVDRNTISYYACAAQLAFFLMFIISEFFILSAMA YDRYVAICNPLL  
 40 YYVIMSQRQLCHVLVGIQYLYSTFQALMFTIKIFLTFCGSNVISHFYCDDVPLLPMLCSNAQIEI  
 LLSILFSVFNLISSFLIVLVSYMLILLAICQMHSAGEGRKKAFTSCGSHLTVVVVFYGSLLFMYMQ  
 PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTCACAGGCGGC  
 45 CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC  
 AACCTAACTATGATCATTTTGACCAAACCTGGACTCCCCTTACATACACCTATGTACTTTTC  
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCAATTTGTCCCAAGGTGCTGG  
 CAAATTTTGTGTGGATCGAAATACTATTTCTTATTATGCATGTGCTGCACAGCTGGCATTC  
 TTCCTTATGTTCAATTATCAGTGAATTTTTCATCCTGTGAGCCATGGCCTATGACCGCTATGT  
 50 GGCCATTTGTAACCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCATGTACTGG  
 TGGGCATTCAATATCTCTACAGCACATTTTCAGGCTCTGATGTTCACTATTAAGATTTTACA  
 TTGACCTTCTGTGGCTCTAATGTCATCAGTCATTTTACTGTGATGATGTTCTTTGCTACC  
 TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAATT  
 TGATCTCCTCCTTTCTGATAGTCTTAGTGTCTACATGTTGATTTGTAGCTATATGTCAA  
 55 ATGATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTCCCATTGACAGTGG  
 TGGTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCACCTCACTTCTTT



GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT  
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA  
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPCALPTGGLLPHQPHTMMEIANVSSPEVFVLLGFSTRPSLETVLFIVVLSFYMVLSILNGNI  
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLG  
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSSTLTMLLPLCG  
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVVLPLGLILVSYGHIARAVLKIRSAEGR  
10 RKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQKGKFIALFYTVVTPALNPLIYTLRNTEVK  
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT  
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCCTCCTGGGCTTCTCCACACGA  
15 CCCTCACTAGAACTGTCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG  
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT  
TTCTTGCCAACCTCCCCTTCTGGACATGAGCTTACCACGAGCATTGTCCCACAGCTCCTG  
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT  
ATCTCCCATTGGCTGGGGGCAACCGAGTGTGTCCTGCTGGCCACCATGTCTATGACCGCT  
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCCTTG  
GCTAGCTTTGGCCTCCTGGCTGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC  
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTTGCGAGATGCCCTCA  
TTATGCAACTGGCTTGTGTGGATAACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT  
TGCTTTTGTTGTCCTGCCTCTGGGGCTCATCCTGGTCTCTTACGGCCACATTGCCCGGGCCG  
25 TGTGAAGATCAGGTGAGCAGAAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCACG  
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG  
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG  
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA  
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30

**AOLFR249 sequences:**

MKSQIEKSDLKYRAILLQKVTRMFLLFWVLLLVLRLVVMGRGNSTEVTEFHLLGFGVQHEF  
QHVLFIIVLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHILAFVDICYTSAITPKMLQSFTEEN  
NLITFRGCVIQFLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQT VYIQLVAGSYIHGSI  
35 NASVHTGFTFSLFCKSNKINHFFCDGLPILALSCSNIDINILDVVFVGFDFLMTLVIIFSITYIM  
VTILKMSSTAGRKKSFSTCASHLTAVTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN  
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGACTTAAAATATAGAGCCATTTTATTGCAAAAAGTC  
40 ACAAGGATGTTCTGCTTTTCTGGGTCCTTCTCTTGGTCCTTTCTAGACTTTTGGTAGTCAT  
GGGTGCGAGGAAACAGCACTGAAGTGACTGAATTCCATCTTCTGGGATTTGGTGTCCAACAC  
GAATTTCAAGCATGTCCTTTTCACTTGTACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA  
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTTC  
CACAACATTTGGCTTTTGTGATATCTGTTATACCTTCTGCTATCACTCCCAAGATGCTCCAA  
45 AGCTTCACAGAAGAAAATAATTGATAACATTTGGGGCTGTGTGATAACAATTCTTAGTTT  
ATGCAACATTTGCAACCAGTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT  
TGCCATCTGTAAGCCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG  
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA  
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTTCTGTGATGGTCTCCCAATTCCTGC  
50 CCTTTCATGCTCCAACATTGACATCAACATCATTCTAGATGTTGTCTTTGTGGGATTTGACT  
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTATGGTCACCATCCTGAAG  
ATGTCTTCTACTGCTGGGAGGAAAAAATCCTTCTCCACATGTGCCTCCACCTGACAGCAG  
TAACCAATTTTCTATGGGACACTCTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG  
GAGAATATGAAAGTAGCCTCTATATTTATGGCACTGTTATCCCATGTTGAATCCTTTAAT  
55 CTATAGCTTGAGAAATAAGGAAGGAAAAATAA (SEQ ID NO: 468).

**AOLFR250 sequences:**

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV  
 DMGLTSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY  
 STVMRPQVCALMLALCWVLTNIVALTHTFLMARLSFCVTGELAHFFCDITPVKLSCSDTHINE  
 5 MMVFLVGGTVLIVPFLCIVTSYIHVPAILRVTRTGGVGKAFSTCSSHL CVV CVFYGTLSAYLC  
 PPSIASEEKDIAAAAMYTIVTPMLNPFYISLRNKDMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGA AAAACCAATCCAGCATTCTGAATTTTCTCCGAGGAATATCAGCGCCTCCAGAGC  
 AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTCACCTTGACTGGGAACCTG  
 10 CTCATCATCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTTCTTGGC  
 CAACCTGTCTTTTGTGACATGGGTTTAACTGCTCCACAGTTACCAAGATGCTGGTGAAT  
 ATACAGACTCGGCATCACACCATCTCCTATACGGGTGCTCAGCAAATGTATTTCTTTCT  
 GATGTTTGGTGATCTAGACAGCTTCTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC  
 ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC  
 15 ATTGTGCTGGGTCTCACC AATATCGTTGCCCTGACTCACACGTTCTCATGGCTCGGTGT  
 CCTTCTGTGTGACTGGGGAAATTGCTCACITTTTCTGTGACATCACTCCTGTCTGAAGCTG  
 TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTGGGAGGCACCGTACTCA  
 TCGTCCCTTTTTATGCATTGTACCTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC  
 CGAACCCGTGGTGGGGTGGGCAAGGCCTTTCCACCTGCAGTTCACCTCTGCGTTGTTT  
 20 GTGTGTTCTATGGGACCCTCTTCAGTGCTACCTGTGTCTCCTCCATTGCCTCTGAAGAG  
 AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT  
 ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA  
 TTGTTCTCTTAG (SEQ ID NO: 470).

**AOLFR251 sequences:**

MEGNKTWITDITLPRFQVGPAL EILL CGLFSAFYTLTLGNGVIFGIICLDCKLHTPMYFFLSHLA  
 IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFAHVECLILVMSYDRYADICHLRY  
 NILMSWRVCTVLAVASWVFSLLALVPLVLILRLPFCGPHEINHFEILSVLKLACADTWLNQV  
 VIFAACVFILVGPLCLVLSYLRLAILRIQS GEGRRKAFSTCSSHL CVV GLFFGSAIVTYMAPK  
 30 SRHPEEQQKVL SLFYSLFNPM LNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA  
 GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACTACCCCTGCTGGGGAA  
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC  
 35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAATATGTCCCAAGATGCTGACG  
 AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT  
 ATTTGGCTTTTGTCTACGTAGAGTGTCTGATTTTGGTGGTGATGTCTATGATCGCTATGCG  
 GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCTCTGG  
 CTGTGGCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT  
 40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT  
 GGCCTGTGCTGACACCTGGCTCAACCAAGTGGTCACTTTGCAGCCTGCGTGTTTCATCCTG  
 GTGGGGCCACTCTGCCTGGTGTCTGCTCTACTTGCGCATCCTGGCCGCCATCTTGAGGA  
 TCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT  
 GGGACTCTTCTTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG  
 45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA  
 TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG  
 AGGCTGACGTGA (SEQ ID NO: 472).

**AOLFR252 sequences:**

MRLANQTLGGDFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL  
 IDLTYSIVTPKMLVNQLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRYVAICHPLR  
 YSVLMSHRVCLLLASGCWVFGSVDGFMLTPIAMSFPCRSH EIQHFFCEVPAVLKLS CSDTSLY  
 KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSHITVVS LFYGA AIYNYML  
 PSSYQTPEKDMMSFFYTILTPVLNPIIYSFRNKDVTRALKKMLS VQKPPY (SEQ ID NO: 473).

55

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCTGTTGGGAATCTTCAGCCAGA  
TCTCACACCCTGGCCGCTCTGCTTGCTTATCTTCAGTATATTTTTGATGGCTGTGCTTGG  
AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT  
TATAAACCAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG  
5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCCTTGGGTGTGGCACCCAGATGTAC  
TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT  
ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC  
CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA  
TGAGCTTCCCCCTTCTGCAGATCCCATGAGATTGAGCACTTCTTCTGTGAGGTCCCTGCTGTT  
10 TTGAAGCTCTCTTGCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT  
CATGCTCCTGATACCTGTGACGGTCATTTTCACTGCTTACTACTATATCATCCTCACCATCC  
ATAAGATGAACTCAGTTGAGGGTCGGAAGGCTTCACCACCTGCTCCTCCACATTAC  
AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACATACATGCTCCCCAGCTCCTACCAA  
ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC  
15 TATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTTGAAAAAATGCTGAGCGT  
GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

#### AOLFR253 sequences:

MTFFSSGGNCEPVMCSGNQTSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNNALL  
20 ILLIHSEPR LHTPMYFFISQLALMDL MYLCVTVPKMLVGQVTGDDTISPSGCGIQMFFHLTLAG  
AEVFLLAAMAYDRYAAVCRPLHYPLLMNQVRVQLLSACWVLGMVDGLLLTPITMSFPFCQS  
RKILSFFCETPALLKLSCSDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLIHRMNSAAGRKA  
LATCSSHMIIVLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTRAL  
RSMQMQRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTTTTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT  
CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTTGCTGAGAGCAAGCA  
TGCTGCCCTCCTCTACACCGTGACCTTCCTTCTTTTCTTGATGGCCCTCACTGGGAATGCCC  
TCCTCATCCTCCTCATCCACTCAGAGCCCCGCCTCCACACCCCCATGTACTTCTTCATCAGC  
30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCAAGATGCTTGTGGGCC  
AGGTCACTGGAGATGATACCATTTCCCCGTCAGGCTGTGGGATCCAGATGTTCTTCCACCT  
GACCCTGGCTGGAGCTGAGGTTTTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT  
GTTTGACAGCCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT  
CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTACCCCCATTACCATGAGCTT  
35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC  
TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT  
CTACCCCCATCATGGTCATCTCCAGCTCATAACCCTCATCTGCATCTCATCCACAGGAT  
GAATTCTGCCGCCGCGCCGAGGAAGGCCTTGGCCACCTGCTCCTCCACATGATCATAGTG  
CTGCTGCTCTTCGGTGCTTCCTTCTACACCTACATGCTCCGGAGTTCTTACCACACAGCTGA  
40 GCAGGACATGATGGTGTCTGCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCCCTCATTT  
ACAGTCTCCGCAACAAAGATGTACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA  
ACCAAGAAAAGTAG (SEQ ID NO: 476).

#### AOLFR254 sequences:

45 MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI  
MDTLFICTTVPKLLADMVSKEKISFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP  
VLMNRKKCLLLAAGAWFGGSLDGFLLPITMNPVPCGSR SINHFFCEIPAVLKLACADTSLYET  
LMYICCVLMLLIPISHSYSILLTIHRMPSAEGRKKAFITCSSHLTVVSIFYGAIFYTVLPQS  
FHTPEQDKVVSIFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACSSAQKVATSDA (SEQ ID NO:  
50 477).

ATGACGAACACATCATCCTCTGACTTCAACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG  
CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCGTGACTGCAAATTTGGT  
CATGATATTCTTGATTGAGGTGGACTCTCGCCTCCACACCCCCATGTACTTTCTGCTCAGTC  
55 AGCTGTCCATCATGGACACCCTTTTATCTGTACCACTGTCCCAAACTCCTGGCAGACAT  
GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT  
 CTGTAACCCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGTCTTTTGCTGGCTGCT  
 GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC  
 CTTACTGTGGCTCCCGAAGTATCAACCATTTTTTCTGTGAGATCCCAGCAGTTCTGAAACT  
 5 GGCCTGTGCAGACACGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGTCTCATGTTG  
 CTCATCCCCATCTCTATCATCTCCACTTCCTACTCCCTCATCTTGTTAACCATCCACCGCAT  
 GCCCTCTGCTGAAGGTCGCAAAAAGGCCTTCACCACTTGTTCCCTCCCACTTGACTGTAGTT  
 AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTTCCACACCCCCG  
 AGCAGGACAAAGTAGTGTACAGCCTTCTATACCATTGTACGCCCATGCTTAATCCTCTCAT  
 10 CTACAGCCTCAGAAACAAGGACGTCATAGGGGCATTTAAAAAGGTATTTGCATGTTGCTCA  
 TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

**AOLFR255 sequences:**

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHDSRLHTPMYFLLSQLS  
 15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH  
 YPVLMSRKICWLIVAAAWLGGSIDGFLLPVTMQPFCASREINHFFCEVPALLKLSCTDTSAY  
 ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT  
 YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTTT (SEQ  
 ID NO: 479).

20 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG  
 CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTGGACCTCCATAGCCAGC  
 AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTCCT  
 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATGTGCCCCAAAATGCTG  
 25 GTCGACAGGTGATGAGCCAGAGGCCATTTCTTTGCTGGATGCACGTGCCCAACACTTCC  
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCCTATGATCGCTAC  
 GTAGCCATCTGCAACCCTCTGCACTATCCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA  
 TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCAT  
 GCAGTCCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC  
 30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT  
 GATGCTCCTCATCCCTTTCTGTCTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT  
 ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG  
 TGGTTGTCAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC  
 ACCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC  
 35 CACTCATTTACAGCCTTAGGAACAAGGATGTCACAGGGGCCCTACAGAAGGTTGTGGGGA  
 GGTGTGTCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

**AOLFR256 sequences:**

MGGKQPWWTEFILVGFQVGPALAILLCGLFSVFYTLTLLGNGVIFGHICLDSKLHTPMYFFLSHL  
 40 AIIDMSYASNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHFP  
 QYTVIMSWRVCTILASTCWISFLMALVHITHILRPPFCGPQKINHFCQIMSVFKLACAGPRLNQ  
 VVLYAGSAFIVEGPLCLELVSNLHLHSRLEDPMGRAADRLTLPAPSHLCMVGLLFGSTMVM  
 YMAPKSRHPPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:  
 481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAAATTCATCCTGGTGGGATTCCAGGTTGGTCCA  
 GCACTGGCGATTCTCCTCTGTGGACTCTTCTCTGTCTTCTATACACTCACCCTGCTGGGGAA  
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC  
 TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC  
 50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG  
 TATTTGGCTTTTGTGTTACAGAGTGCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT  
 GGCCATCTGCCACCCCTTCCAGTACACTGTATCATGAGCTGGAGAGTGTGCACGATCTCTGAG  
 GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATCTGAG  
 GCCGCTTTTGTGGCCCAAAAAGATCAACCACTTATCTGTCAAATCATGTCCTGATTCA  
 55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCCTATATGCGGGTTCTGCGTTTCAT  
 CGTAGAGGGCCGCTCTGCCTGGAGCTGGTCTCCCACTTGACATCCTGTGCGCCATCTT

GAGGATCCAGTAATGGGGAGGGCCGCAGACCGACTTACTCTTCCTGCTCCTTCCCACCTTT  
 GCATGGTGGGACTCCTTTTTGGCAGCACCATGGTCATGTACATGGCCCCCAAGTCCCGCCA  
 CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC  
 CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCCTGAAAAGAGTGTTGTGG  
 5 AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

**AOLFR257 sequences:**

MESNQTWITEVILLGFQVDPALELFLFGFFLLFYSLTLMGNGIILGLIYLDRLHTPMYVFLSHL  
 AIVDMSYASSTVPMKLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMCYDRYVAICHPL  
 10 QYTLIMNWRVCTVLASTCWIFSLLALVHTLILRLPFCGPQKINHFFCQIMSVFKLACADTRLN  
 QVVLFAFSFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM  
 APKSSHSQERRKILSLFYSLFNPILNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA  
 15 GCTCTGGAGTTGTTCTCTTTGGGTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA  
 TGGGATTATCCTGGGGCTCATCTACTGGACTCTAGACTGCACACCCCATGTATGTCTTC  
 CTGTCACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG  
 CAAATCTTGTGATGCACAAAAAGTCATCTCCTTTGCTCCTTGCCATACTTCAGACTTTTTTG  
 TATTTGGCGTTTGCTATTACAGAGTGCTGATTTTGGTGATGATGTGCTATGATCGGTATG  
 20 TGGCAATCTGTCACCCCTTGAATACACCCTCATTATGAACTGGAGAGTGTGCACTGTCTC  
 GGCTCAACTTGCTGGATATTTAGCTTTCTCTGGCTCTGGTCCATATTACTCTTATTCTGA  
 GGCTGCCTTTTTGTGGCCCAAAAAGATCAACCACCTTTTCTGTCAAATCATGTCCGTATTC  
 AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCTCTATTGCGGGTTCTGCGTTCA  
 TCTTAGTGGGGCCGCTCTGCCTGGTGCTGGTCTCCTACTTGACACATCCTGGTGGCCATCTTG  
 25 AGGATCCAGTCTGGGGAGGGCCGCAGAAAGGCCTTCTCTACCTGCTCCTCCACCTCTGCG  
 TGGTGGGGCTTTTTCTTTGGCAGCGCCATTGTCATGTACATGGCCCCCAAGTCAAGCCATTC  
 TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC  
 CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTGGAAA  
 CAGAGATCAATGTGA (SEQ ID NO: 484).

30

**AOLFR259 sequences:**

MGDNQSRVTEFILVGFQLSVEMEVLLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL  
 AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVMSYDRFVAICHPL  
 HYTVIMNWRVCTVLAITSWACGFSLLALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN  
 35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY  
 LVPDNSQRQKQKILTLFYSLFNPILNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:  
 485).

ATGGGGGACAACCAATCACGGGTCACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG  
 40 GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAAA  
 TGGCATGATCTTGGGGCTCATCTGTCTGGATCCCAGACTGCGCACCCCCATGTACTTCTTCC  
 TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA  
 AAACCTAGTGAAACACAAAAAACTATCTCGTTTCATCTCTTGCAATTATGCAGATGGCTTTG  
 TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTTGT  
 45 GCGGATCTGCCATCCCCTGCATTACACTGTCATCATGAACTGGAGAGTGTGCACAGTACTG  
 GCTATTACTTCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG  
 GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTCTGTCTGTCTC  
 AAAGTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTCTTTGCTGGTGGTGTGTTTG  
 TCTTAGTCGGGCCCCCTTTCTTGATGCTGATCTCCTACATGCGCATCCTCTTGCCATCCTG  
 50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAGCCTTTTCCACCTGCTCCTCCCACCTCTGTG  
 TGGTTGGGCTTTACTTTGGCATGGCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG  
 ACAGAAGCAGCAGAAAATTCTCACCCCTGTTTACAGCCTTTTCAACCCATTTGCTGAACCCC  
 CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA  
 AAGAGGACCATGTGA (SEQ ID NO: 486).

55

**AOLFR24B sequences:**

MPSINDTHFYPPFFLLGIPGLDTHLWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM  
 LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMETVLLVVMAYDRFVAICNP  
 LQYTMILTNTKISILASVVVGRNLVLVTPFVFLILRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN  
 5 IYGLMVISYIIVDVILIASYVLILRAVFRPLSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH  
 RFGQNIPHYIHILLANLYVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCTCCTGCTAGGAATACCAGG  
 ACTGGACACTTTACATATCTGGATTTCTTTCCCATTCTGTATTGTGTACCTGATTGCCATTG  
 10 TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATGTT  
 CTACTTCCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA  
 TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT  
 GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC  
 GCTTTGTTGCCATCTGCAACCCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG  
 15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAAACCCCATTTGTGTTTCTCA  
 TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG  
 TCTGGCCGGGTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT  
 TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCCTATGTGCTTATCCTTAGAGCTGT  
 TTTTCGCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT  
 20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTTCTTTTATGACACATCGTTTTGGCCAA  
 AACATTCCCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCACCTGCCCT  
 TAACCCTGTCAATTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT  
 GTACAGAAAGAATAA (SEQ ID NO: 488)

**AOLFR33B sequences:**

MLHTNNTQFHPSTFLVVGVPGLDVHVWIGFPFFAVYLTALLGNIIILFVIQTEQSLHQPMFYFL  
 AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTHICTGLESVVLTVTGIDRYAICNP  
 LRYSMILTNTKVIALGIVIVRTL VFVTPFTFLTLRLPFCGVRIIPHTYCEHMGALAKLACASINVY  
 GLIAFSVGYIDISVIGFSYVQILRAVFLPAWDARLKALSTCGSHVCVMLAFYLPALFSFMTHRF  
 30 GHNPPIHYIHILLANLYVVFPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ  
 (SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCTTCCACCTTCTCCTAGTAGTGGGGGTCCCAG  
 GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT  
 35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG  
 TTTTACTTCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA  
 AGATGCTGGGAATTTTCTGGTTTAATCTTGGAGAGATTGCATTGGTGCCTGCATCACACA  
 GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA  
 GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA  
 40 TAGCCATTCTGGGCATAGTCATCATTGTGAGGACTTTGGTATTTGTGACTCCATTACATTT  
 CTCACCCTGAGATTGCCTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT  
 GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA  
 GTGGGATACATTGACATTTCTGTGATTGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT  
 CCATCTCCCAGCCTGGGATGCCCGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT  
 45 GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTTCTTTCATGACACACCGCTTTGGCCACAA  
 CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCTGCTCTTA  
 ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA  
 ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTAGTTAGACA  
 ATAA (SEQ ID NO: 490)

50

**AOLFR112B sequences:**

MKNKTVLTEFILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILTLTLDLQTPMYFFLRNFSF  
 LEISFTNIFIPVLISITGKNKSISFAGCFTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI  
 MSSRIQILFCSWLGGMLMAIPTITLMSQQDFCASNRLNHYFCDYEPLLELSCSDTSLIEKVVFL  
 55 VASVTLVVTLLVLSYAFIITILKLPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG  
 DTFNKGVALLITSVAPLLNPFYITLRNQVQKQPKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC  
 TCCAGGTGGCAGTTTTACCTTTCTTTTCCCTGCGTATTTACTCAGCATCCTTGGAAATCTG  
 ACTATCCTCATCCTCACCTTGCTGGACTCCCACCTTCAGACTCCCATGTATTTCTTTCTCCG  
 5 GAACCTTCTCCTTCTTGGAATTTCTTTCACAAACATCTTCATTCCAAGGGTCTGATTAGCA  
 TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT  
 GTTCCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC  
 ATCTGCAAAACCTCTGCATTACACCACCATCAGCAGCAGAATCTGCATCCAGCTGATTT  
 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA  
 10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA  
 CTCTCATGTTTCAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTGGCATCTGTGACCC  
 TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTCATTATCAAGACTATTCTGAAG  
 CTCCCCTCTGCCCAACAAAGGACAAAAGCCTTTTCCACATGTTCTTCCCACATGATTGTCAT  
 CTCCCCTCTTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAAGAAGGGGAT  
 15 ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT  
 TTACACCCTAAGGAACCAACAGGTAAAACAACCCTTCAAGGATATGGTCAAAAAGCTTCT  
 GAATCTTTAA (SEQ ID NO: 492)

**AOLFR130B sequences:**

20 MEGKNQTAPSEFIILGFDHLNELQYLLFTIFFLTYICTLGGNVFIHVVTIADSHLHTPMYYFLGNL  
 ALIDICYTTTNPVQMMVHLLSEKKIISYGGCVTQLEAFIFVVGSECLLLAAMAYDRYIAICKPLR  
 YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFLPFCGNNQINFFCDIPPLLILSCGDTSLNE  
 LALLSIGILISWTPFLCHLSYLIIISTILIRSSSEGRHKAFSTCASHLLVILYYGSAIFTYVRPISSYS  
 LEKDRLLISVLVSVVTPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)  
 25  
 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTTCGACCACCTGA  
 ATGAATTGCAGTATTTACTCTTACCATCTTCTTTCTGACCTACATATGCACTTTAGGAGGC  
 AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCCACCTACACACACCCATGTATTATTT  
 CCTAGGAAATCTTGGCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG  
 30 GTGCATCTTCTGTGAGAGAAGAAAATCATTTCCTATGGAGGCTGTGTGACCCAGCTCTTTG  
 CATTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT  
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTATTTATTATGAACAAGGCCCTGTGCAGCTGGT  
 TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT  
 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC  
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACTGGCTTTGCTGTCCATTGGGATCCTC  
 ATAAGCTGGACTCCTTTCCCTGTGCATCCTTTCCCTACCTTTACATCATCTCCACCATCCT  
 GAGGATCCGTTCCCTCTGAGGGGAGGCACAAAGCCCTTTCCACCTGTGCCTCCCACTGCTC  
 ATTGTTATTCTCTATTATGGCAGTGCTATCTTACCGTATGTGAGGCCATCTCATCTTACTC  
 TCTAGAGAAAAGATAGATTGATCTCAGTGCTGTATAGTGTGTGCACACCCATGCTGAATCCT  
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG  
 TGGCAGCCACCAGTTTTCTTCTGATATATAA (SEQ ID NO: 494)

**AOLFR142B sequences:**

45 MARKDMAHINCTQATEFILVGLTDHQLKMPFLVFLSIYLFVVGNLGLILLIRADTSLNTPM  
 YFFLSNLA FVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLASMA YDRY  
 VAICNPLLYMVVMT PGICQLVAVPYSYSFLMALFHTILTFRLSYCHSNIVNHFYCD DMPLRL  
 TCS DTRFKQLWIFACAGIMFISSLLIVFVS YMFII SAILRMHSAEGRQKAFSTCGSHMLAVTIFYG  
 TLIFMYLQ PSSSHALD TDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIINKN (SEQ ID NO:  
 495)  
 50  
 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG  
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC  
 TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA  
 CACCAATGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTTCTGTTACTCTTCTGTCATT  
 55 ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG  
 CTACTCAACTGGGCTGCTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG



GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG  
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTAC  
 ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCAATTTCTATTGTGA  
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT  
 5 GCCTGTGCTGGTATCATGTTCAATTTCCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTTCATC  
 ATTTCTGCCATCCTGAGGATGCATTAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG  
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTATGTACTTACAGCCT  
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC  
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA  
 10 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

#### AOLFR171C sequences:

MAEVNIIVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL  
 AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLASMAFYDCYVAICSPL  
 15 HYSTLMSTRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLNHFYCDLPLALSCSDTHMK  
 EILIFAFAGFDMISSSIVLTSYIFILAILRIRSTQGQHKAISTCGSHMVTVTIFYGTLIFMYLQPKS  
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ  
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCTGAAAGGAATTACCAACCGGC  
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTTAGTTATCTATCTGGTCACAGTGCTGGG  
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT  
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG  
 GTGAATTTTGTGTGGAACGCAACACCATTCCTTTCCATGCTTGTGCAACCCAACTGGGTT  
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCCTTCTAGCCTCCATGGCCTACGATTGCTAT  
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC  
 TGGTGGCAGTTCCATATATATACAGCTTCTGTTGCCCTCTTCCACACCGTTATCACTTTT  
 CGTCTGACTTACTGTGGCCAACTTAATTAACCATTTCTATTGTGATGACCTCCCCTTCTT  
 AGCTCTGTCTGCTCAGACACACACATGAAGGAAATTCTGATATTGCTTTGCTGGCTTT  
 30 GATATGATCTCTTCTCCTCTTCCATTGTCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA  
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCCACCTGTGGCTCCCATATGGTGA  
 CTGTCACTATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC  
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC  
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG  
 35 GTTGTGAAAACCTACAGATATTAACATTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:  
 498)

#### AOLFR225B sequences:

MKNRTMFGFILLGLTNQPELQVMIFLFLTYMLSILGNLTIITLTLDDPHLQTPMYFFLRNFSF  
 40 LEISFTSIFIPRLTSMTTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI  
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYCDYGPLVELACSDTSLLELMVI  
 LLAVVTLMTLVLTLSYTYIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKE  
 GGAFNKGIAVLITSVTPLLNPFYITLRNQVKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC  
 TCCAAGTGATGATATTCATCTTTCTGTTCTCACCTACATGCTAAGTATCCTAGGAAATCTG  
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCTCCG  
 GAATTTCTCCTTCTTAGAAATTTCTTACATCCATTTTATTCCCAGATTTCTGACCAGCA  
 TGACAAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTGTCTAT  
 50 ATTTCTTGGAGCTACCGAGTTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA  
 TCTGCAAACCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACTAGTGTT  
 CTGCTCCTGGTTGGGGGGATTCTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA  
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT  
 TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC  
 55 ATGGTTACTCTGGTGCTGGTGACACTTCTTACACATACATTATCAGGACTATTCTGAGGA  
 TCCCTTCTGCCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCTCTCCACATGATTGTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG  
 CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTACTCCCTTACTGAATCCCTTCATA  
 TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG  
 AAACCTTTAA (SEQ ID NO: 500)

5

**AOLFR274B sequences:**

MEFVFLAYPSCPHELHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV  
 VVPHILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLMLTLTL  
 CVHLVVASVISGLFSLQLVAFISLPFCQAQGIEHFFCDVPPVMHVCAQSHIHEQSVLVAAIL  
 10 AIAVPFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ  
 DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTCTGGCCTATCCCTCCTGCCAGAACTGCATATTCTGTCCTTCCTTGG  
 GGTCAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC  
 15 ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGCAGCCTTTCTGGGATTGAAA  
 TATGCTACACTGCAGTGGTGGTGCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC  
 CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGTGAT  
 TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTGCCCACCGTTGCAGTA  
 CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC  
 20 TGTTCTGTCTTACAACCTGGTGGCCTTCATCTTCTCTGCCATTCTGCCAGGCTCAGGGC  
 ATTGAGCACTTCTTTGTGATGTGCCACCACTCATGCATGTTGTTGTGCTCAGAGTCACAT  
 TCATGAGCAGTCAGTGTGTGGCAGCCATACTAGCCATTGCTGTGCTTCTTCTCCTCATC  
 ACCACCTCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTTCTGCGCCGCC  
 ACCGGGCCTTCTCCACCTGCTCTTCCACCTCACTGTGGTGCTGCTGCAGTATGGCTGCTGT  
 25 GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC  
 TGGTGTACACATTGGGAACCCCACTGCTCAACCCACTTATCTATGCCCTGAGGAACAGTGA  
 GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAACTGCCTTTCCCAGAACAGCTAG  
 (SEQ ID NO: 502)

30 **AOLFR276B sequences:**

MGGFGTNISSTTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIIKEEQSLHQPMYYFLS  
 LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFHDHYVAICNP  
 LRYATVLT DVRVAHNGISIVIRSF CMVFPLPFLKRLPFCKASVVLAHSYCLHADLIRLPWGD  
 TINS MYGLFIVISAFGVDSLILLSYVLILHSVLAIASRGERLKT LNTCVSHIYAVLIFYVPMVSVS  
 35 MVHRFRGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG  
 AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCCCTT  
 40 CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGCACCAGCCAATG  
 TACTACTTCCTGTCTCTTTTTTCTGTAAATGACCTGGGTGTGTCCTTTTCTACATTGCCCACT  
 GTACTGGCTGCTGTGTGTTTTTCATGCCCCAGAGACAACCTTTGATGCCTGCCTGGCCCAGA  
 TGTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTTGAC  
 CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG  
 45 CCCACAATGGCATATCCATTGTCTATCCGCACTTCTGCATGGTATTCCCACTTCCCTTCTC  
 CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCTACTGTCTGCATG  
 CAGACCTGATTGCGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTCAT  
 TGTCTCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTCTAC  
 ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC  
 ACATATCTATGCAGTGTGATCTTCTATGTGCCTATGGTTAGTGTGTCCATGGTTTCATCGAT  
 50 TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTGTACCTCCAATGCTCT  
 ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

**AOLFR311B sequences:**

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINF SANLGMIVLIRMDYQLHTPMYFFLS  
 55 HLSFCDCLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLSVMAFDYKAIINP  
 LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLLSRSDTQV

NELVLFTVFGFIELSTISGVFISYCYILSVLEIHS AEGRFKALSTCTSHLSAVAIFQGTLLFMYFRP  
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTTTCTCTTGGGAATTACCAATAACCC  
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTTATATCATTAATTTCTCAGCAA  
ATCTTGGAATGATAGTTTTAATCAGAATGGATTACCAACTTACACACCAATGTATTTCTT  
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCCAAGATGCTGG  
TAGATCTACTTGCCAAGAACAAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTCTTGGT  
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTCAGTGATGGCCTTTGATCGGTACA  
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT  
CTTGAAGTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC  
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT  
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTTATTCACCGTCTTTGGTTTA  
TTGAACTGAGTACCATTTAGGAGTTTTCATTTCTTATTGTTATATCATCCTATCAGTCTTG  
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTCTACATGCACTTCCCACTTATCTG  
CGGTTGCAATTTTCCAGGGAAGTCTGCTCTTTATGTATTTCCGGCCAAGTCTTCTCCTATTCT  
CTAGATCAAGATAAAATGACCTCATTGTTTTACACCCTTGTGGTTCCCATGTTGAACCCCT  
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT  
TTATTTTAA (SEQ ID NO: 506)

20

**AOLFR314 sequences:**

MEVKNCCMVTEFILLGIPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG  
NLSVDFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFHFLGSIECFLFTVMAFYDRFTAICY  
PLRYTVIMNPRICVALAVGTWLLGCIHSSILTSFTLPYCGPNEVDHFFCDIPALLPLACADTSL  
25 AQRVSFTNVGLISLVCFLLILLSYTRITISILSIRTTEGRRRAFSTCSAHLIAILCAYGPIITVYLQPT  
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCCACACACA  
GAGGGGCTGGAGATGACACTTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG  
30 AAATGTGTCTATCCTTGTGTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT  
TCCTGGGAAACTTGTCTGTGTTGACATGGGTTTCTCCTCAGTGACTTGTCCAAAATGCT  
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT  
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTTGTTTACGGTGATGGCCTATGACCGCTTC  
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC  
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCATTCAATCCAGTATCTTGACCTCCCTCACCTTC  
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT  
GCCCTTGGCCTGTGCTGACACATCCTTAGCCAGAGGGTGAGCTTCACCAACGTTGGCCTC  
ATATCTCTTGTCTGCTTTCTGCTAATTCTTTTATCCTACACTAGAAATCACAATATCTATCTT  
AAGCATTGTAACAAGTGGGGCCGTCGCCGTGCCTTCTCCACCTGCAGTGCTCACCTCATT  
40 GCCATCCTCTGTGCTATGGGCCCATCATCACTGTCTACCTGCAGCCCAACCCCAACCCCA  
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT  
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG  
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

**AOLFR324B sequences:**

MPIANDTQFHTSSFLLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYYCLA  
MLDSIDLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFVMEIVLVAMAFDRYIAICKPL  
WYTMILTSKIISLIAGIAVLRSLYMPIVLVFLRLPFCGHRIIPHTYCEHMGARLACASIKVNM  
FGLGSISLILLDLVLLIILSHIRLYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH  
50 DIPQYIHIFLANLYVVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCATACTTCTTCATTCTCTACTGCTGGGTATCCCAGG  
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC  
TGGGAAATGCTGCTATCTTCTTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTA  
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTCCTCAA  
ATGCTGGGCATCTTCTGGTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTTCTCAGA

TGTTCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC  
CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA  
GCCTCATTGCAGGCATTGCTGTCCTGAGGAGCTTGACATGGTCATTCCACTGGTGTCT  
CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG  
5 GCATTGCCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT  
TTCTCTCTTGTTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT  
CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT  
GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTTCTCTTTCTTTACACACTGCTTTGGCCAT  
GATATCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCTCCACCCT  
10 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC  
TTCAAGACAGATCACTAA (SEQ ID NO: 510)

**AOLFR328 sequences:**

MALGNHSTITEFLLLGLSADPNIRALLFVLFGLIYLLTIMENLMLLLVRADSCLHKPMYFFLSH  
15 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVVTAGTEACLLSGMAYDRHAAIRRP  
LLYGQIMGKQLYMHLVWGSWGLGFLDALINVLLAVNMVFEAKIIHHYSYEMPSLLPLSCSDI  
SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL  
MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC  
CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTTGGGGATTACCTCCTGACCATAATGGA  
AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGCTCCATAAGCCCATGTATTTCT  
TCCTGAGTCACCTCTCTTTGTTGATCTCTGCTTCTCTTCAGTCATTGTGCCCAAGATGCTG  
GAGAACCTCCTGTCACAGAGGAAAACCATTTAGTAGAGGGCTGCCTGGCTCAGGTCTTCT  
25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA  
TGCTGCCATCCGCCGCCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC  
CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCTCCTAGCTG  
TAAACATGGTCTTTTGTGAAGCCAAAATCATTACCACTACAGCTATGAGATGCCATCCCT  
CCTCCCTCTGTCCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGCTCTGCTCCACTCTCC  
30 TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC  
CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCACCTCA  
CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCCGCCATCTCATGCCAAACTCAGGTTT  
CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCTCA  
TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGGAAAAATATT  
35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)

Claims:

1. A method for representing sensory perception of one or more odorants comprising:
  - 5 (a) providing a representative class of  $n$  olfactory receptors or ligand-binding domains thereof;
  - (b) measuring values  $X_1$  to  $X_n$  representative of at least one activity of the one or more odorants selected from the group consisting of binding of the one or more odorants to the ligand-binding domain of at least one of the  $n$  olfactory receptors, activating at least one of the  $n$  olfactory receptors with the one or more odorants, and blocking at least one of the  $n$  olfactory receptors with the one or more odorants; and
  - 10 (c) generating a representation of sensory perception from the values  $X_1$  to  $X_n$ ;
- 15 wherein at least one of the  $n$  olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169,
- 20
- 25
- 30

SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID  
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5 SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID  
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10 NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259,  
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15 SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID  
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20 NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349,  
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25 SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID  
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SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID  
5 NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:  
511.

2. The method of Claim 1, wherein at least one of the olfactory receptors  
specifically recognizes the odorant, and there are between 5 and 350 of the n olfactory  
10 receptors selected from the listed amino acid sequences.

3. The method of Claim 1, wherein at least two different activities are measured  
to provide the values  $X_1$  to  $X_n$ .

15 4. The method of Claim 1, wherein each odorant receptor is expressed in cells,  
and the cells expressing each odorant receptor are located at an identifiable position.

5. The method of Claim 1, wherein at least one olfactory receptor is soluble, and  
binding of odorant to a ligand-binding domain of the soluble olfactory receptor is  
20 measured in solution.

6. The method of Claim 1, wherein at least one olfactory receptor is in solid state,  
and binding of odorant to a ligand-binding domain of the solid-state olfactory receptor  
is measured on a substrate.  
25

7. The method of Claim 1, wherein the value measured for binding is above a  
preset limit for specific binding to olfactory receptors.

8. The method of Claim 1, wherein the value measured for activating an olfactory  
30 receptor is derived from a signal selected from the group consisting of intracellular  
 $Ca^{2+}$ , cAMP, cGMP and IP3.



9. The method of Claim 1, wherein the value measured for activating an olfactory receptor is above a preset limit for specific activation.
10. The method of Claim 1, wherein the value measured for blocking an olfactory  
5 receptor is at least a reduction in binding of the odorant or activation by the odorant.
11. The method of Claim 1, wherein the representation of sensory perception is generated with a neural network.
- 10 12. A biosensor comprised of the n ligand-binding domains or olfactory receptors of Claim 1.
13. A method for producing a database of odorant representations comprising:  
(a) providing one or more known odorants and  
15 (b) generating a representation of the one or more known odorants in accordance with the method of Claim 1 to produce the database.
14. A database produced by Claim 13.
- 20 15. A method of identifying an unknown odorant comprising:  
(a) measuring values  $X_1$  to  $X_n$  representative of at least one activity selected from the group consisting of binding the unknown odorant to a ligand-binding domain of at least one of n olfactory receptors, activating at least one of n olfactory receptors with the unknown odorant, and blocking at  
25 least one of n olfactory receptors with the unknown odorant;  
(b) generating a representation of the unknown odorant from the values  $X_1$  to  $X_n$ ; and  
(c) comparing the unknown odorant's representation to the database of Claim 14 to identify the known odorant which is most similar in  
30 representation.
16. A method of producing an artificial odorant comprising:

- 5 (a) measuring values  $X_1$  to  $X_n$  representative of at least one activity selected from the group consisting of binding a desirable odorant to a ligand-binding domain of at least one of  $n$  olfactory receptors, activating at least one of  $n$  olfactory receptors with a desirable odorant, and blocking at least one of  $n$  olfactory receptors with a desirable odorant;
- (b) generating a representation of the desirable odorant from the values  $X_1$  to  $X_n$ ;
- (c) decomposing the desirable odorant's representation into representations of known odorants from the database of Claim 14 or  
10 superposing known odorants' representations from the database to reproduce the desirable odorant; and
- (d) formulating the known odorants to reproduce sensory perception of the desirable odorant and thereby produce the artificial odorant.

15 17. An artificial odorant produced by Claim 16.

18. A method of identifying a primary odorant related to sensory perception comprising:

- 20 (a) providing a representative class of  $n$  olfactory receptors or ligand-binding domains thereof,
- (b) measuring at least one activity of a odorant selected from the group consisting of binding of the candidate odorant to the ligand-binding domain of at least one of the  $n$  olfactory receptors and activating with the candidate odorant at least one of the  $n$  olfactory receptors, and
- 25 (c) identifying the candidate odorant as a primary odorant if only one or less than 10% of the representative class of  $n$  olfactory receptors is bound or activated;

wherein at least one of the  $n$  olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID  
30 NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID

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30 SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID  
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19. A primary odorant identified by Claim 18.

20. A method of identifying a compound which blocks activation by a odorant of at least one olfactory receptor comprising:

- 25 (a) producing a structurally-related candidate compound from a ligand of the at least one olfactory receptor,
- (b) measuring activation by the odorant of the at least one olfactory receptor with the candidate compound, and
- (c) identifying the candidate compound as a compound which blocks
- 30 activation if activation of the at least one olfactory receptor is reduced or inhibited;

wherein at least one of the olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID

NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID  
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25 21. The method of Claim 20, wherein the ligand is a primary odorant.

22. A compound which blocks activation of an olfactory receptor identified by Claim 20.